GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2003, 17:18:00 ; Search time 267 Seconds
(without alignments)
2111.528 Million cell updates/sec

Title: US-09-494-297-2
Perfect score: 3945
Sequence: 1 MKKTRFPNKLNTLNTQRVLS.....IAGISLGIWGIHTIRIRKHD 757

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 738101 seqs, 372376393 residues

Total number of hits satisfying chosen parameters: 1476202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Pending_Patents_NA_New -QFMT=fastap -SUFFIX=rnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	149	3.8	3945	5	US-09-200-650E-6	Sequence 6, Appli
	2	142	3.6	2976	6	US-10-615-383-7	Sequence 7, Appli
	3	136.5	3.5	2841	5	US-09-200-650E-4	Sequence 4, Appli
	4	134.5	3.4	5310	6	US-10-617-320-1073	Sequence 1073, Ap
	5	134	3.4	1683	6	US-10-333-002-18	Sequence 18, Appl
	6	131.5	3.3	4593	1	PCT-US02-37235-43	Sequence 43, Appl
	7	131	3.3	4371	1	PCT-US03-22113-28	Sequence 28, Appl
	8	131	3.3	5043	6	US-10-450-826-5	Sequence 5, Appli
	9	130	3.3	3371	7	US-60-490-890-1650	Sequence 1650, Ap
c	10	129.5	3.3	8514	6	US-10-623-500-12	Sequence 12, Appl
c	11	129.5	3.3	8692	6	US-10-623-500-13	Sequence 13, Appl
	12	129	3.3	4925	6	US-10-450-826-4	Sequence 4, Appli
	13	128	3.2	4226	6	US-10-105-837-480	Sequence 480, App
	14	128	3.2	4226	6	US-10-286-897-796	Sequence 796, App
	15	128	3.2	4226	6	US-10-258-898A-796	Sequence 796, App
c	16	128	3.2	1830121	6	US-10-329-670-1	Sequence 1, Appli
	17	127	3.2	17734	7	US-60-479-073-499	Sequence 499, App
	18	126	3.2	4026	1	PCT-US03-22113-2	Sequence 2, Appli
	19	126	3.2	4183	1	PCT-US03-22113-1	Sequence 1, Appli
	20	126	3.2	6450	1	PCT-US03-22113-27	Sequence 27, Appl
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	22	124	3.1	1917	5	US-09-674-546A-2160	Sequence 2160, Ap
	23	124	3.1	2604	5	US-09-674-546A-2166	Sequence 2166, Ap
	24	124	3.1	6429	6	US-10-603-108-1539	Sequence 1539, Ap
	25	124	3.1	11116	6	US-10-286-897-1473	Sequence 1473, Ap
	26	124	3.1	11116	6	US-10-258-898A-1473	Sequence 1473, Ap
	27	123.5	3.1	3450	5	US-09-662-254B-47	Sequence 47, Appl
	28	123.5	3.1	11657	6	US-10-357-930-23435	Sequence 23435, A
	29	123.5	3.1	11657	6	US-10-357-930-29321	Sequence 29321, A
	30	123.5	3.1	50000	5	US-09-662-254B-25	Sequence 25, Appl
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	32	121.5	3.1	1923	6	US-10-603-113-4780	Sequence 4780, Ap
	33	121.5	3.1	11013	6	US-10-273-573-3047	Sequence 3047, Ap
	34	120.5	3.1	2433	6	US-10-603-113-6178	Sequence 6178, Ap
	35	120.5	3.1	2712	6	US-10-333-002-9	Sequence 9, Appli
	36	120	3.0	2196	6	US-10-603-113-3972	Sequence 3972, Ap
	37	120	3.0	2412	6	US-10-603-114-714	Sequence 714, App
	38	120	3.0	4205	6	US-10-286-897-326	Sequence 326, App
	39	120	3.0	4205	6	US-10-258-898A-326	Sequence 326, App
	40	119.5	3.0	1746	6	US-10-603-113-1302	Sequence 1302, Ap
	41	119.5	3.0	13320	1	PCT-US02-39397-124	Sequence 124, App
	42	119	3.0	1584	6	US-10-603-113-1814	Sequence 1814, Ap
	43	119	3.0	7990	6	US-10-273-573-3051	Sequence 3051, Ap
	44	119	3.0	12499	6	US-10-273-573-3045	Sequence 3045, Ap
	45	119	3.0	12500	6	US-10-273-573-3048	Sequence 3048, Ap

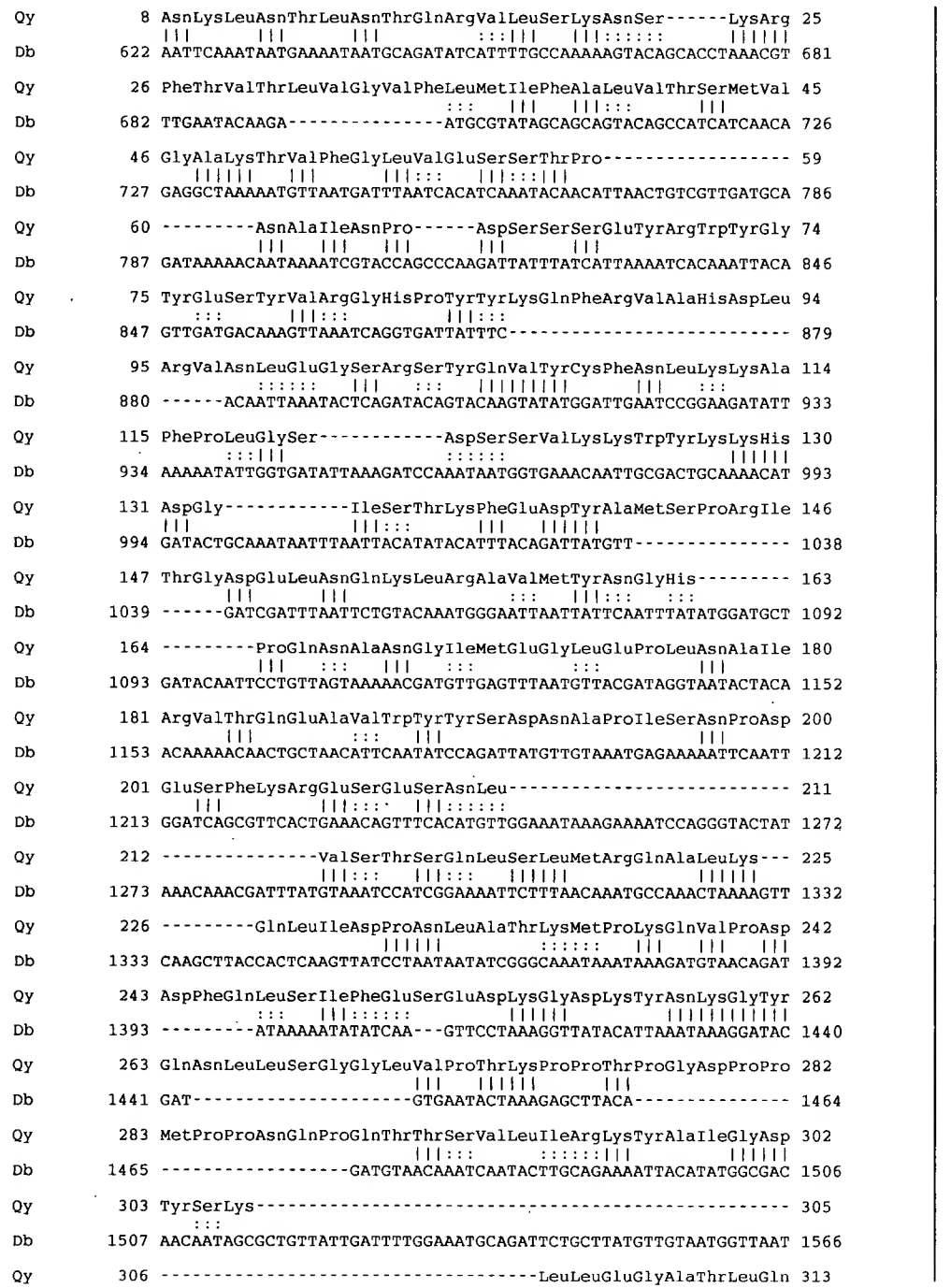
ALIGNMENTS

RESULT 1
US-09-200-650E-6
; Sequence 6, Application US/09200650E
; GENERAL INFORMATION:
; APPLICANT: Patti, Joseph M.
; APPLICANT: Foster, Timothy J.
; APPLICANT: Hook, Magnus A.O.
; APPLICANT: Eidhinn, Deirdre Ni
; APPLICANT: Perkins, Samuel L.
; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aure
; FILE REFERENCE: P06283US2/BAS
; CURRENT APPLICATION NUMBER: US/09/200,650E
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,815
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/098,427
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 3945
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-200-650E-6

Alignment Scores:

Pred. No.:	9.65e-09	Length:	3945
Score:	149.00	Matches:	203
Percent Similarity:	29.48%	Conservative:	93
Best Local Similarity:	20.22%	Mismatches:	336
Query Match:	3.78%	Indels:	372
DB:	5	Gaps:	45

US-09-494-297-2 (1-757) x US-09-200-650E-6 (1-3945)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Qy 147 ThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMetTyrAsnGlyHis--------- 163
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Qy 164 ---------ProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAlaIle 180
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Qy 212 ---------------ValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLys--- 225
Db 1273 AAACAAACGATTTATGTAAATCCATCGGAAAATTCTTTAACAAATGCCAAACTAAAAGTT 1332
Qy 226 ---------GlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAsp 242
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Qy 303 TyrSerLys-- 305
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Qy 306 ----------------------------------LeuLeuGluGlyAlaThrLeuGln 313
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Qy 314 LeuThrGlyAsp-- 317
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Qy 318 --AsnVal 319
Db 1687 GGCGGAGCTGGTCAAGAAGTATATAAAATTGGTAACTACGTATGGGAAGATACTAATAAA 1746
Qy 320 AsnSerPheGln--------------------------------AlaArgValPheSer 328
Db 1747 AACGGTGTTCAAGAATTAGGAGAAAAAGGCGTTGGCAATGTAACTGTAACTGTATTTGAT 1806
Qy 329 SerAsn---------AspIleGlyGluArgIleGluLeuSerAspGlyThrTyrThrLeu 345
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Qy 346 ThrGluLeu--------------------------AsnSerProAlaGlyTyrSer 355
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Qy 385 Ile---------------------ValGluProTyrSerValGluAlaTyrAsnAspPhe 397
Db 2227 GTTGAATTTACTACACCAGAAGGCTATACACCGACTACAGTAACATCTGGTAGCGACATT 2286
Qy 398 GluGluPheSer---ValLeuThrThrGlnAsnTyr----------------------- 408
Db 2287 GAAAAAGACTCTAATGGTTTAACAACAACAGGTGTTATTAATGGTGCTGATAACATGACA 2346
Qy 409 ------AlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValValTyrCys 426
Db 2347 TTAGATAGTGGATTCTACAAAACACCAAAATATAATTTAGGTAATTATGTATGGGAAGAT 2406
Qy 427 PheAsnAlaAspLeuLysSerProProAspSerGluAsp---------GlyGlyLysThr 443
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Qy 444 MetThrProAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAsp--- 462
Db 2461 GTTACATTGAAAAATGAAAACGGTGAAGTTTTACAAACAACTAAAACAGATAAAGATGGT 2520
Qy 463 LeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHisIle 482
Db 2521 AAATATCAATTTACT-- 2535
Qy 483 LysLysValIleGluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyr--------- 499
Db 2536 ------------------GGATTAGAAAATGGAACTTATAAAGTTGAATTCGAAACACCA 2577
Qy 500 SerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIle---TyrTyrPhe 518

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Db       2578 TCAGGTTACACACCAACACAAGTAGGTTCAGGAACTGATGAAGGTATAGATTCAAATGGT 2637

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Db       2638 ACATCAACAACAGGTGTCATTAAAGATAAAGATAACGATACTATTGACTCTGGTTTCTAC 2697

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Qy        567 PheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAsp 586
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Qy        605 AsnLeuThrLeuArgLys--------------ThrValThrGlyLeu---------Ala 616
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Db       2938 GGAAATGATACTGAAAAAGATTCTAATGGTTTAACAACAACAGGTGTCATTAAAGATGCA 2997

Qy        617 GlyAspArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeu 636
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RESULT 2
US-10-615-383-7
; Sequence 7, Application US/10615383
; GENERAL INFORMATION:
;  APPLICANT: FOSTER, Timothy
;  TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLC
;  FILE REFERENCE: P06335US03/BAS
;  CURRENT APPLICATION NUMBER: US/10/615,383
;  CURRENT FILING DATE:  2003-07-09
;  PRIOR APPLICATION NUMBER: 09/386,962
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: 60/098,443
;  PRIOR FILING DATE: 1998-08-31
;  PRIOR APPLICATION NUMBER: 60/117,119
;  PRIOR FILING DATE: 1999-01-25
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 2976
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3)..(2975)
;   OTHER INFORMATION:
US-10-615-383-7

Alignment Scores:
Pred. No.:              5.3e-08      Length:          2976
Score:                  142.00       Matches:         164
Percent Similarity:     34.88%       Conservative:    130
Best Local Similarity:  19.45%       Mismatches:      320
Query Match:            3.60%        Indels:          231
DB:                     6            Gaps:            41

US-09-494-297-2 (1-757) x US-10-615-383-7 (1-2976)

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Db        165 ATTAGAAAATTCACAGTAGGTACAGCGTCTATT-------------------------- 197

Qy         43 SerMetValGlyAlaLysThrValPheGlyLeu-----------------ValGluSer 56
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Db        198 ---GTAATAGGTGCAGCATTATTGTTTGGTTTAGGTCATAATGAGGCCAAAGCTGAGGAG 254

Qy         57 SerThrProAsnAlaIleAsnProAspSerSerSerGluTyrArgTrpTyrGlyTyrGlu 76
              ::::||          :::      ||||||:::   :::
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Qy        136 LysPheGluAspTyrAlaMetSer---------------------------------- 143
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Qy        164 ProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAlaIleArgValThr 183
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Db        549 GTCGAATCCTCAAATTCATCAATGGATACTGCCCAACAACCATCTCATACAACAATAAAT 608

Qy        184 GlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsn---ProAspGluSer 202
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Db        609 AGTGAAGCATCTATTCAAACAAGTGATAATGAAGAAAATTCCCGCGTATCAGATTTTGCT 668

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                    :::      |||||||||      |||      :::   :::   :::   |||
Db        669 AACTCTAAAATAATAGAGAGTAACACTGAATCCAATAAAGAAGAGAATACTATAGAGCAA 728

Qy        223 AlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAsp 242
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Db        729 ----------------------------------------CCTAACAAAGTAAGAGAA 746
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Qy        243 AspPheGlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyrAsnLysGlyTyr 262
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Qy        263 GlnAsnLeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPro 282
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Db        858 TTATCTACAACATCTGCCCAACCATCGAGTAAGCGTGTAACCGTAAATCAATTAGCGGCA 917

Qy        301 GlyAspTyrSerLysLeuLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsn 320
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Qy        321 SerPheGlnAlaArgValPheSerSerAsnAspIleGlyGluArgIleGluLeuSerAsp 340
Db        939 CATTTAATTAAA------GTTACTGATCAAAGTATTACTGAAGGATATGATGATAGTGAT 992

Qy        341 GlyThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIle 360
Db        993 GGTATTATTAAAGCACATGATGCTGAAAACTTAATC---TATGATGTAACTTTTGAAGTA 1049

Qy        361 ThrPheLysValGluAlaGlyLysValTyrThrIle---IleAspGlyLysGlnIle--- 378
Db       1050 GATGATAAGGTGAAATCTGGTGATACGATGACAGTGAATATAGATAAGAATACAGTTCCA 1109

Qy        378 ------------------------------------------------------------ 378
Db       1110 TCAGATTTAACCGATAGTTTTGCAATACCAAAAATAAAAGATAATTCTGGAGAAATCATC 1169

Qy        379 ---------------GluAsnProAsnLysGluIleValGluProTyrSer------Val 391
Db       1170 GCTACAGGTACTTATGACAACACAAATAAACAAATTACCTACACTTTTACAGATTATGTA 1229

Qy        392 GluAlaTyrAsnAspPheGluGluPheSerValLeuThrThrGlnAsnTyrAlaLysPhe 411
Db       1230 GATAAATATGAAAATATTAAAGCGCACCTTAAATTAACATCA------------------ 1271

Qy        412 TyrTyrAlaLysAsnLys------AsnGlySerSerGlnValValTyrCysPheAsnAla 429
Db       1272 TACATTGATAAATCAAAGGTTCCAAATAATAACACTAAGTTAGATGTAGAATATAAGACG 1331

Qy        430 AspLeuLysSerProProAspSerGluAspGlyGlyLysThrMetThrProAspPhe--- 448
Db       1332 GCCCTTTCATCAGTA-----------------AATAAAACAATTACGGTTGAATATCAA 1373

Qy        449 ---------------ThrThrGlyGluValLys------TyrThrHisIleAlaGlyArg 461
Db       1374 AAACCTAACGAAAATCGGACTGCTAACCTTCAAAGTATGTTCACAAACATA--------- 1424

Qy        462 AspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHis 481
Db       1425 GATACGAAAAACCATACAGTT---------------GAGCAAACGATTTATATTAACCCT 1469

Qy        482 IleLysLysValIleGluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyrSerGly 501
Db       1470 CTTCGT-----------------TATTCAGCCAAAGAAACAAATGTAAATATTTCAGGG 1511

Qy        502 LeuThrGlu---------ThrGlnLeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPhe 518
Db       1512 AATGGCGATGAAGGTTCAACAATTATCGACGATAGTACAATCATTAAAGTTTATAAGGTT 1571

Qy        519 ThrAspSerAlaGluLeu---AspLysAspLysLeuLysAspTyrHisGlyPheGlyAsp 537
Db       1572 GGAGATAATCAAAATTTACCAGATAGTAACAGAATTTATGATTACAGTGAATATGAAGAT 1631

Qy        538 MetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsn 557
Db       1632 GTCACAAATGAT-------------------------GATTATGCCCAA--------- 1655

Qy        558 ProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeu 577
Db       1656 ----------------------------TTAGGAAATAATAATGACGTGAATATTAAT 1685

Qy        578 IleGlyThrGlnTrpHisProGluAspLeuValAspIleIleArgMetGluAsp------ 595
Db       1686 TTTGGTAATATAGATTCACCATAT---ATTATTAAAGTTATTAGTAAATATGACCCTAAT 1742

Qy        596 LysLysGluValIleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeu 615
Db       1743 AAGGACGATTACACGACGATACAGCAAACTGTGACAATGCAAACGACTATAAATGAGTAT 1802

Qy        616 AlaGly--------------------AspArgThrLysAspPheHisPheGluIleGlu 628
Db       1803 ACTGGTGAGTTTAGAACAGCATCCTATGATAATACAATTGCTTTCT--CTACAAGTTCAG 1860

Qy        629 LeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeu 648
Db       1861 GTCAAGGACAAGGTGACTTGCCTCCTGAAAAAACTTATAAAATCGGAGATTACGTA-TGG 1919

Qy        649 GluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGluSer------------ 664
Db       1920 GAAGATGTAGATAAAGATGGTATTCAAAATACAAATGATAATGAAAAACCGCTTAGTAAT 1979

Qy        665 ---LeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAspSer 683
Db       1980 GTATTGGTAACTTTGACGTATCCTGATGGAACTTCAAAATCAGTCAGA---ACAGATGAA 2036

Qy        684 GluGly-------------------------------------TyrLysValLysValAsn 691
Db       2037 GAGGGAAATATCAATTTGATGGGTTAAAAAACGGATTGACTTATAAAATTACATTCGAA 2096

Qy        692 SerGlnGluValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGluThrLeu 711
Db       2097 ACACCGGAAGGATATACGCCGACGCTTAAACATTCAGGA------ACAAATCCTGCACTA 2150

Qy        712 AlaPheGluAsnAsnLysGluProValValProThrGlyValAspGlnLysIleAsnGly 731
Db       2151 GACTCAGAAGGCAATTCTGTATGGGTAACT--------------------ATTAACGGA 2189

Qy        732 TyrLeuAlaLeuIleValIleAlaGlyIle-----------------SerLeuGly--- 744
Db       2190 CAAGACGATATGACTATTGATAGCGGATTTTATCAAACACCTAAATATAGCTTAGGGAAC 2249

Qy        745 ---IleTrp 746
Db       2250 TATGTATGG 2258
```

RESULT 3
US-09-200-650E-4
; Sequence 4, Application US/09200650E
; GENERAL INFORMATION:
; APPLICANT: Patti, Joseph M.
; APPLICANT: Foster, Timothy J.
; APPLICANT: Hook, Magnus A.O.
; APPLICANT: Eidhinn, Deirdre Ni
; APPLICANT: Perkins, Samuel L.
; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aure
; FILE REFERENCE: P06283US2/BAS
; CURRENT APPLICATION NUMBER: US/09/200,650E
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,815
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/098,427
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2841
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-200-650E-4

Alignment Scores:

Pred. No.:	2.8e-07	Length:	2841
Score:	136.50	Matches:	135
Percent Similarity:	31.39%	Conservative:	80
Best Local Similarity:	19.71%	Mismatches:	254
Query Match:	3.46%	Indels:	216
DB:	5	Gaps:	29

US-09-494-297-2 (1-757) x US-09-200-650E-4 (1-2841)

```
Qy         95 ArgValAsnLeuGluGlySerArgSerTyrGlnVal--TyrCysPheAsnLeuLysLysA 114
              |||:::|||          |||   |||   |||  ||||||||||||
Db         49 CGATTAAACAAATTTTCGATAAGAAAGTATTCTGTAGGTACTGCTTCAATTTT------- 101

Qy        114 laPheProLeuGlySerAspSerSerValLysLysTrpTyrLys-LysHisAspGlyIle 133
                       |||      ::::::      |||   |||    |||:::
Db        102 --------------AGTAGGGACAACATTGATTTTTGGGTTAAGTGGTCATGAA------ 141

Qy        134 SerThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGln 153
                          |||   :::         |||      ||||||||||||
Db        142 --------------------GCTAAAGCGGCAGAACATACGAATGGAGAATTAAATCAA 180

Qy        154 LysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGly 173
                                      :::   |||       :::
Db        181 TCAAAAAATGAAACGACA-----------GCCCCAAGTGAGAATAAAACAACTAAAAAA 228

Qy        174 LeuGluProLeuAsnAlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsn 193
              ::::::                    ||||||   |||           :::|||
Db        229 GTTGATAGTCGTCAACTAAAAGACAATACGCAAACTGCAACT---------GCAGATCAG 279

Qy        194 AlaProIleSerAsnProAspGluSerPheLysArgGluSerGluSerAsnLeuValSer 213
                  ::::::      |||   :::      :::|||:::   ||||||:::   |||
Db        280 CCTAAAGTGACAATGAGTGATAGTGCAACAGTTAAAGAAACTAGTAGTAACATGCAATCA 339

Qy        214 ThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAla 233
                  :::   :::
Db        340 CCACAAAACGCTACAGCTAATCAATCT----------------------------ACT 369

Qy        234 ThrLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSerGluAsp 253
              ||||||                 :::|||         :::   :::   :::|||
Db        370 ACAAAAACTAGCAATGTAACAACAAATGATAAATCATCAACTACATATAGTAATGAAACT 429

Qy        254 LysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValProThr 273
                 ||||||                 ||||||          |||   |||
Db        430 ------GATAAA--------------AGTAATTTAACACAAGCAAAAGATGTTTCAACT 468

Qy        274 LysProProThrProGlyAspProProMetProProAsnGlnProGlnThrThrSerVal 293
                 |||   |||          |||         |||:::              :::|||
Db        469 ACACCTAAAACAACGACTATTAAACCAAGAACTTTAAATCGCATGGCAGTGAATACTGTT 528

Qy        294 LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeuGluGlyAlaThrLeuGln 313
                    :::
Db        529 GCAGCTCCACAA---------------------------------------------- 540

Qy        314 LeuThrGlyAspAsnValAsnSerPheGlnAlaArgVal---PheSerSerAsnAspIle 332
                 |||   |||||||||            :::|||   ||||||:::   ||||||
Db        541 ---CAAGGAACAAATGTTAATGAT---------AAAGTACATTTTTCAAATATTGACATT 588

Qy        333 GlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGlu--------------- 347
                          :::   |||         ||||||
Db        589 GCGATTGATAAAGGACATGTTAATCAGACTACTGGTAAAACTGAATTTTGGGCAACTTCA 648

Qy        348 ---------LeuAsnSerProAlaGlyTyrSerIleAlaGluProIle------------ 360
                    |||         |||   |||:::|||   :::   :::
Db        649 AGTGATGTTTTAAAATTAAAAGCAAATTACACAATCGATGATTCTGTTAAAGAGGGCGAT 708

Qy        361 ------ThrPheLys------------ValGluAlaGlyLysValTyrThrIleIleAsp 374
                    ||||||||               |||   |||
Db        709 ACATTTACTTTTAAATATGGTCAATATTTCCGTCCAGGATCAGTAAGATTACCTTCACAA 768

Qy        375 GlyLysGlnIleGluAsnProAsnLysGluIleValGluProTyrSerValGluAlaTyr 394
                 :::   :::   |||          |||:::          :::          |||
Db        769 ACTCAAAATTTATATAATGCCCAAGGTAATATTATT---------GCAAAAGGTATTTAT 819

Qy        395 AsnAspPheGluGluPheSerValLeuThrThrGlnAsnTyrAlaLysPheTyr------ 412
              :::             :::       |||       ||||||          |||
Db        820 GATAGTACAACAAACACAACAACATATACTTTTACGAACTATGTAGATCAATATACAAAT 879

Qy        413 --------------------------TyrAlaLysAsnLysAsnGlySerSer---Gln 422
                                        :::||||||   ||||||   ::::::   :::
Db        880 GTTAGAGGTAGCTTTGAACAAGTTGCATTTGCGAAACGTAAAAATGCAACAACTGATAAA 939

Qy        423 ValValTyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAsp--------- 439
                    |||               |||   :::         ||||||:::
Db        940 ACAGCTTATAAAATGGAAGTAACTTTAGGTAATGATACATATAGCGAAGAAATCATTGTC 999

Qy        440 ------GlyGlyLysThrMetThrProAspPheThrThrGlyGluValLysTyrThrHis 457
                    |||   |||         |||      ::::::
Db       1000 GATTATGGTAATAAAAAAGCACAACCGCTTATTTCAAGTACAAACTATATTAACAATGAA 1059

Qy        458 IleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThr---AspProAsp 476
                  |||::::::      |||      :::|||:::::::|||
Db       1060 GATTTATCGCGTAATATGACTGCATATGTAAATCAACCTAAAAATACATATACTAAACAA 1119

Qy        477 ThrPheLeuLysHisIleLysLysValIleGluLysGlyTyrArgGluLysGlyGlnAla 496
              ||||||:::   ::::::                 ||||||:::            |||
Db       1120 ACGTTTGTTACTAATTTA--------------ACTGGATATAAATTTAATCCAAATGCA 1164

Qy        497 IleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIleTyr 516
                  :::                                                ||||||
Db       1165 AAAAACTTCAAA-------------------------------------------ATTTAC 1182

Qy        517 TyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPheGly 536
                  ||||||      :::
Db       1183 GAAGTGACAGATCAAAATCAATTT---------------------------------- 1206

Qy        537 AspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSer 556

Db       1206 ---------------------------------------------------------- 1206

Qy        557 AsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSer 576
                                      :::|||   |||   |||:::   :::|||   :::
Db       1207 --------------------GTGGATAGTTTCACCCCTGATACTTCAAAACTTAAAGAT 1245

Qy        577 LeuIleGlyThrGlnTrpHisProGluAspLeuValAspIleIleArgMetGluAspLys 596
                  :::                        |||      |||:::|||       |||
Db       1246 GTT--------------------ACTGATCAATTCGATGTTATTTATAGTAATGATAAT 1284

Qy        597 LysGluValIleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeuAla 616
                 |||                 |||      :::   |||   |||    |||
Db       1285 AAA---------------ACAGCTACAGTCGATTTAATGAAAGGCCAAACA--------- 1320

Qy        617 GlyAspArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeu 636
                                                        :::||||||||   :::
Db       1321 -------------------------------------AGCAGCAATAAACAATACATC 1341

Qy        637 LeuSerGln-----------------------------------------------Thr 640
                  :::   |||                                           |||
Db       1342 ATTCAACAAGTTGCTTATCCAGATAATAGTTCAACAGATAATGGAAAAATTGATTATACT 1401

Qy        641 ValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLys 660
                  :::   ||||||||||||       :::  :::      :::   :::|||
Db       1402 TTAGACACTGACAAAACTAAATATAGTTGGTCAAATAGTTATTCAAATGTGAAT------ 1455

Qy        661 HisGlyGluSerLeuThrLeuGlnGlyLeuProGluGlyTyrSer---------TyrLeu 677
                       |||   |||      |||      :::   |||:::          |||:::
Db       1456 ------GGCTCATCAACTGCTAATGGCGACCAAAAGAAATATAATCTAGGTGACTATGTA 1509

Qy        678 ValLysGluThrAspSerGluGlyTyrLysValLysValAsnSerGlnGluValAlaAsn 697
                 ::::::|||:::   :::|||   |||         |||   :::   :::
Db       1510 TGGGAAGATACAAATAAAGATGGT---AAACAAGATGCCAATGAAAAAGGGATTAAAGGT 1566

Qy        698 AlaThrVal---------SerLysThrGlyIleThrSerAspGluThrLeuAlaPheGlu 714
                  |||             |||         |||   |||          |||
Db       1567 GTTTATGTCATTCTTAAAGATAGTAACGGTAAAGAATTAGATCGTACGACAACAGATGAA 1626
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Qy        715 AsnAsnLys 717
              |||   |||
Db       1627 AATGGTAAA 1635

RESULT 4
US-10-617-320-1073
; Sequence 1073, Application US/10617320
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
;                            SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE   FOR DIAGNO
;                            THERAPEUTICS
;        NUMBER OF SEQUENCES: 5206
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: <Unknown>
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: <Unknown>
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/617,320
;             FILING DATE: 10-Jul-2003
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,433
;             FILING DATE: 30-Jun-1998
;             APPLICATION NUMBER: 60/ 085131
;             FILING DATE: May 12, 1998
;             APPLICATION NUMBER: 60/051553
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-011
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 1073:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5310 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Streptococcus pneumoniae
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...5310
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1073:
US-10-617-320-1073

Alignment Scores:
Pred. No.:              1.71e-06      Length:        5310
Score:                  134.50        Matches:       161
Percent Similarity:     31.52%        Conservative:  112
Best Local Similarity:  18.59%        Mismatches:    268
Query Match:            3.41%         Indels:        325
DB:                     6             Gaps:          43

US-09-494-297-2 (1-757) x US-10-617-320-1073 (1-5310)

Qy        145 ArgIleThrGlyAspGluLeuAsnGlnLys---LeuArgAlaValMet------------ 159
              :::::|||   |||   :::      |||   |||:::|||||||:::
Db        988 AAGGTGACTTATGATACGATCCAGTCTAAGGTACTTAAGGCAGTAATTGACCAAGCCTTC 1047

Qy        160 --------------------TyrAsnGlyHisPro--------------GlnAsnAla 167
                                  |||||||||                  |||
Db       1048 CCTCGTGTCAAGGAATACACCTTGAATGGACATACTTTGCCAGGACAGGTGCAACAATTC 1107

Qy        168 AsnGlyIleMetGluGlyLeuGluProLeuAsnAlaIleArgValThrGlnGluAlaVal 187
              |||   :::                  :::|||      |||:::|||   |||   |||
Db       1108 AACCAAGTCTTT--------------ATCAATAACCACCGAATCACCCCTGAA---GTC 1149

Qy        188 TrpTyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerPheLysArgGluSer 207
               |||         |||        :::      :::        |||
Db       1150 ACTTATAAAAAAATCAATGAG------ACAACAGCAGAGTACTTGATGAAGCTTCGCGAT 1203

Qy        208 GluSerAsnLeuValSer---------ThrSerGlnLeuSerLeuMetArgGlnAlaLeu 224
              :::::::::|||::::::         |||   :::|||   ::::::        |||
Db       1204 GATGCTCACTTAATCAATGCGGAAATGACAGTACGCTTGCAAGTTGTGGACAATCAATTG 1263

Qy        225 -----------LysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnVal 240
                         ::::::::::::   |||      |||      |||   |||
Db       1264 CACTTTGATGTGACCAAGATTGTCAACCACAATCAAGTCACT------CCAGGTCAAAAG 1317

Qy        241 ProAspAspPheGln-----------------------------------LeuSerIle 248
              ||||||   :::                                      |||
Db       1318 ATTGATGACGAAAGAAAACTACTTTCTTCTATTAGTTTCCTCGGCAATGCTTTAGTCTCT 1377

Qy        249 PheGluSerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGly 268
              |||:::      |||   |||::::::                            |||
Db       1378 GTTTCTAGTGATCAAACTGGTGCTAAGTTTGAT-----------------------GGG 1413

Qy        269 GlyLeuValProThrLysProProThrProGlyAspProProMetProProAsnGlnPro 288
              :::                      ||||||      :::            |||
Db       1414 GCAACCATGTCAAACAATACGCATGTCAGCGGAGATGATCATATCGATGTAACCAATCCA 1473

Qy        289 GlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSer------LysLeu 306
                        |||   :::  |||      |||      |||      ||||||
Db       1474 ATGAAGGAT------TTGGCTAAGGGTTACATGTATGGATTTGTTTCTACAGATAAGCTT 1527

Qy        307 LeuGluGlyAlaThrLeuGlnLeuThr---------------GlyAspAsn--------- 318
              |||                                     |||   |||
Db       1528 GCTGCTGGTGTTTGGAGTAACTCTCAAAATAGCTATGGTGGTGGTTCGAATGACTGGACT 1587

Qy        319 ---ValAsnSerPheGlnAlaArgValPheSerSerAsnAspIleGly------------ 333
                 :::   :::::::::      |||   :::::::|||   :::|||
Db       1588 CGTTTGACAGCTTATAAAGAAACAGTCGGAAATGCCAACTATGTAGGAATCCACAGCTCT 1647

Qy        333 ------------------------------------------------------------ 333

Db       1648 GAATGGCAATGGGAAAAAGCTTATAAGGGCATTGTTTTCCCAGAATACACGAAGGAACTT 1707

Qy        334 ----------------------------------------GluArgIleGluLeuSer 339
                                                     ::::::::::::
Db       1708 CCAAGTGCTAAGGTTGTTATCACTGAAGATGCCAATGCAGACAAGAAAGTTGATTGGCAA 1767

Qy        340 AspGlyThrTyrThrLeuThrGlu---LeuAsnSerProAlaGlyTyrSerIleAlaGlu 358
              ||||||                  :::|||:::|||   |||:::         :::
Db       1768 GATGGTGCCATTGCTTATCGTAGCATTATGAACAACCCTCAAGGTTGGGAAAAAGTTAAG 1827

Qy        359 ProIleThrPheLysValGluAlaGlyLysValTyrThrIleIle------AspGlyLys 376
              ||||||                        |||   |||           |||
Db       1828 GATATCACA--------------------GCTTACCGTATCGCGATGAACTTTGGTTCT 1866

Qy        377 GlnIleGluAsnPro------------------------------------------- 381
              |||   :::|||||||
Db       1867 CAAGCACAAAACCCATTCCTTATGACCTTGGATGGTATCAAGAAAATCAATCTCCACACA 1926

Qy        382 -----------AsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAsp--- 396
                        :::::::::   |||      |||   ::::::
Db       1927 GATGGTCTTGGGCAAGGTGTTCTCCTTAAAGGATATGGTAGCGAAGGCCATGACTCTGGT 1986

Qy        397 ------------------------------------PheGluGluPheSerValLeu 403
                                                  |||:::|||      |||
Db       1987 CACTTGAACTATGCTGATATTGGTAAGCGTATCGGTGGTGTCGAAGACTTCAAGACCCTA 2046

Qy        404 ThrThrGlnAsnTyrAlaLysPheTyr------------------------------- 412
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Db       2047 ATTGAGAAG------GCTAAGAAATATGGAGCTCATCTAGGTATCCACGTTAACGCTTCA 2100

Qy        413 ------TyrAlaLysAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAsp 430

Db       2101 GAAACTTATCCTGAGTCTAAATACTTCAATGAAAAAATTCTC------------------- 2142

Qy        431 LeuLysSerProProAspSerGluAspGlyGlyLysThrMetThrProAspPheThrThr 450

Db       2143 CGTAAGAATCCAGATGGAAGCTATAGCTATGGTTGGAACTGGCTAGATCAAGGTATCAAC 2202

Qy        451 GlyGluValLysTyrThrHisIleAlaGlyArg---------------AspLeuPheLys 465

Db       2203 ATTGATGCTGCCTATGACCTAGCTCATGGTCGTTTGGCACGTTGGGAAGATTTGAAGAAA 2262

Qy        466 TyrThrValLysProArgAsp---------------------------------Thr 473

Db       2263 AAACTTGGTGACGGTCTCGACTTTATCTATGTGGACGTTTGGGGTAATGGTCAATCAGGT 2322

Qy        474 AspProAspThrPheLeuLysHisIle------LysLysValIleGluLysGlyTyrArg 491

Db       2323 GATAACGGTGCCTGGGCTACCCACGTTCTTGCTAAAGAAATTAACAAACAAGGCTGGCGC 2382

Qy        492 ---------GluLysGlyGlnAla---------------------------------- 496

Db       2383 TTTGCGATCGAGTGGGGCCATGGTGGTGAGTACGACTCTACCTTCCATCACTGGGCAGCT 2442

Qy        497 ---IleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIle 515

Db       2443 GACTTGACCTACGGTGGCTACACCAATAAAGGTATCAACAGTGCCATCACCCGCTTTATC 2502

Qy        516 TyrTyrPheThrAspSerAla---------------------------------------- 522

Db       2503 CGTAACCACCAAAAAGATGCTTGGGTTGGGGACTACAGAAGTTATGGTGGTGCAGCCAAC 2562

Qy        523 ------GluLeuAspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMetAsnAsp 540

Db       2563 TATCCACTGCTAGGTGGCTACAGCATGAAAGACTTTGAAGGCTGGCAAGGAAGAAGTGAT 2622

Qy        541 ---------------SerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGln--- 554

Db       2623 TACAATGGCTATGTAACCAACTTATTTGCCCATGACGTCATGACTAAGTACTTCCAACAC 2682

Qy        555 ---------------------AspSerAsnProProGlnLeuThrAspLeuAspPhePhe 567

Db       2683 TTCACTGTAAGTAAATGGGAAAATGGTACACCGGTGACTATGACCGAT------------ 2730

Qy        568 IleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAspLeu 587

Db       2731 ------AACGGTAGCACCTAT-----------------AAATGGACTCCAGAAATGCGA 2766

Qy        588 ValAspIleIleArgMetGluAspLysLysGluValIle---------------ProVal 602

Db       2767 GTGGAATTGGTAGATGCTGACAATAATAAAGTAGTTGTAACTCGTAAGTCAAATGATGTC 2826

Qy        603 ThrHisAsnLeuThrLeuArgLysThrValThr--------------------------- 613

Db       2827 AATAGCCCACTATACCGTGAACGTACAGTAACGCTCAACGGACGTGTCATCCAAGATGGT 2886

Qy        614 ----------------------------------------GlyLeuAlaGlyAspArg 619

Db       2887 TCAGCTTACTTGACTCCTTGGAACTGGGATGCAAATGGTAAGAAACTTTCTACTGATAAG 2946

Qy        620 ThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeu--------- 636

Db       2947 GAAAAGATGTACTACTTCAATACGCAGGCCGGTGCAACAACTTGGACCCTTCCAAGCGAT 3006

Qy        637 ----------------------------LeuSerGlnThrValLysThrAspLysThr 646

Db       3007 TGGGCAAAGAGCAAGGTTTACCTTTACAAGCTAACTGACCAAGGTAAGACAGAAGAGCAA 3066

Qy        647 AsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGluSerLeuThr 666

Db       3067 GAACTAACTGTAAAAGATGGTAAAATTACCCTAGATCTTCTAGCAAATCAACCATACGTT 3126

Qy        667 LeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAsp------------ 682

Db       3127 CTC------------------------TATCGTTCGAAACAAACCAATCCTGAAATGTCA 3162

Qy        683 ---SerGluGly---------TyrLysValLysValAsnSerGlnGluValAlaAsnAla 698

Db       3163 TGGAGTGAAGGCATGCACATCTATGATCAAGGATTTAATAGCGGTACTTTGAAACATTGG 3222

Qy        699 ThrVal------------SerLysThrGlyIleThr------------SerAspGluThr 710

Db       3223 ACCATTTCAGGCGATGCTTCTAAGGCAGAAATTGTCAAGTCTCAAGGGGCAAACGATATG 3282

Qy        711 LeuAlaPheGluAsnAsnLysGluProVal---------------------------- 720

Db       3283 CTTCGTATTCAAGGAAACAAAGAAAAAGTTAGTCTCACTCAGAAATTAACTGGCTTGAAA 3342

Qy        721 -----------------ValProThrGlyValAspGlnLysIleAsnGlyTyrLeuAla 734

Db       3343 CCAAATACCAAGTATGCCGTTTATGTCGGTGTCGATAACCGTAGTAATGCCAAGGCAAGT 3402

Qy        735 LeuIleValIleAlaGly 740

Db       3403 ATCACTGTGAAATACTGGT 3420
```

RESULT 5
US-10-333-002-18
; Sequence 18, Application US/10333002
; GENERAL INFORMATION:
; APPLICANT: Adderson, Elisabeth
; APPLICANT: Bohnsack, John
; TITLE OF INVENTION: Group B Streptococcus Polypeptides Nucleic Acids and Therapeut
; TITLE OF INVENTION: Compositions and Vaccines Thereof
; FILE REFERENCE: 2511-1-001 (SJ-0039)
; CURRENT APPLICATION NUMBER: US/10/333,002
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/US01/24795
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 09/634,341
; PRIOR FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
US-10-333-002-18

Alignment Scores:

Pred. No.:	2.33e-07	Length:	1683
Score:	134.00	Matches:	103
Percent Similarity:	33.81%	Conservative:	40
Best Local Similarity:	24.35%	Mismatches:	130
Query Match:	3.40%	Indels:	150
DB:	6	Gaps:	26

US-09-494-297-2 (1-757) x US-10-333-002-18 (1-1683)

```
Qy        386 ValGluProTyr---SerValGluAlaTyrAsnAspPheGluGluPheSerValLeuThr 404

Db        214 GTTAATCCATATGGTAGTATTAGACCTTATAAC------------TTTTCAGGTGCTGTA 261

Qy        405 ThrGln------AsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGln 422

Db        262 ACTCAAGATATCAATTTAAGAGCTATTTGG---------CGAAAGGCTGGAGATTATCAT 312

Qy        423 ValValTyrCysPheAsnAla---------AspLeuLysSerProProAspSerGluAsp 439

Db        313 ATTATATACAGCAATGATGCTGTTGGTACAGATGGAAAGCCAGCATTGGATGCT---TCT 369

Qy        440 GlyGlyLysThrMetThrProAspPheThrThrGlyGluValLysTyrThrHisIleAla 459
```

```
Db        370 GGTCAGCAATTACAAACAAGTAATGAGCCTACTGACCCTGATTCCTATGACGATGGCTCC 429

Qy        460 GlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeu 479
                  |||   :::              |||  |||   ||||||
Db        430 CATTCAGCCTTACTGAGA--------------CGTCCGACAATGCCAGAT--------- 465

Qy        480 LysHisIleLysLysValIleGluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyr 499
                                  |||||||||   :::|||           |||
Db        466 --------------------------GGCTATCGTTTCCGTGGCTGG------TGGTAC 492

Qy        500 SerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPheThr 519
              :::|||                                  ||||||
Db        493 AATGGT-----------------------------------AAAATTTATAACCCATAT 516

Qy        520 AspSerAlaGluLeuAspLysAsp---------------------------------- 527
              ||||||   ::::::|||
Db        517 GATTCCATTGATATTGACGCCCATTTAGCAGATGCTAATAAAAATATCACCATAAAACCT 576

Qy        528 ----------------------LysLeuLysAsp-----------TyrHisGlyPhe 535
                                   ||||||:::|||           |||:::|||
Db        577 GTCATTATTCCAGTAGGAGATATCAAATTAGAAGATACCTCCATCAAATACAATGGTAAC 636

Qy        536 GlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAsp 555
              |||                    |||                        |||
Db        637 GGTGGTACTAGAGTAGAAAATGGTAATGTGGTA-----------------ACACAAGTG 678

Qy        556 SerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyr--- 574
                 |||          :::          ||||||  |||    :::
Db        679 GAGACACCGCGTATGGAGTTGAATAGCACAACTACAATTCCTGAAAACCAATACTTTACA 738

Qy        575 ---------GlnSerLeuIleGlyThrGlnTrp---HisProGluAspLeuValAspIle 590
                    :::||||||||||      |||  |||  :::||||||   |||
Db        739 AGGACAGGTTACAACCTTATTGGT------TGGCATCATGATAAGGATTTAGCTGATACA 792

Qy        591 IleArgMetGlu-------------------------------------AspLysLys 597
              |||:::|||                                      |||
Db        793 GGACGTGTGGAATTTACAGCAGGTCAATCAATAGGTATTGATAACAACCTTGATGCAACA 852

Qy        598 GluValIle---------------ProValThrHisAsnLeuThrLeuArgLysThrVal 612
                 :::              |||      :::  :::   :::  |||||||||
Db        853 AATACCTTATATGCTGTTTGGCAACCTAAAGAATACACCGTCGGAGTAAGTAAAACTGTC 912

Qy        613 ThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsn 632
              ||||||      |||:::|||||||||||||   |||                 |||
Db        913 GTTGGACTAGATGAAGATAAGACGAAAGACTTCTTGTTT-----------------AAT 954

Qy        633 LysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPheLysAsp 652
                 |||   |||   |||                    |||         :::|||
Db        955 CCAAGTGAAACGTTGCAACAA-----------------GAGAATTTTCCGCTGAGAGAT 996

Qy        653 GlyLysAlaThrIleAsnLeuLysHisGlyGluSerLeuThrLeuGlnGlyLeuProGlu 672
              |||:::   |||         |||                        :::|||
Db        997 GGTCAG---ACTAAGGAATTTAAA-------------------------GTACCTTAT 1026

Qy        673 GlyTyrSerTyrLeuValLysGluThrAspSerGluGlyTyrLysValLysValAsnSer 692
              |||   |||      :::   |||         :::   :::|||||      :::
Db       1027 GGAACTTCTATATCAATAGATGAACAAGCCTACGATGAATTTAAAGTATCTGAGTCAATT 1086

Qy        693 GlnGlu-----------------ValAlaAsnAlaThrValSerLysThrGlyIleThr 706
                 |||                  |||:::   |||         ||||||:::
Db       1087 ACAGAAAAAAATCTAGCAACTGGTGAAGCTGATAAAACTTATGATGCTACCGGCTTACAA 1146

Qy        707 Ser---------------AspGluThrLeuAlaPheGluAsnAsnLysGluProValVal 721
              |||              |||      :::::::|||   |||
Db       1147 TCCCTGACAGTTTCAGGAGACGTAGATATTAGCTTTACCAAT----------------- 1188

Qy        722 ProThrGlyValAspGlnLysIle----------------------------AsnGly 731
                 |||   :::   ||||||:::                          |||
Db       1189 ---ACACGTATCAAGCAAAAAGTACGACTACAGAAAGTTAATGTCGAAAATGATAATAAT 1245

Qy        732 TyrLeuAla 734
              :::||||||
Db       1246 TTTTTAGCA 1254
```

```
RESULT 6
PCT-US02-37235-43
; Sequence 43, Application PC/TUS0237235
; GENERAL INFORMATION:
;  APPLICANT: Handfield, Martin
;  APPLICANT:  Hillman, Jeffrey
;  APPLICANT:  Progulske-Fox, Ann
;  TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans Antigen
;  TITLE OF INVENTION:  in the Diagnosis, Treatment, and Monitoring of Periodontal Di
;  FILE REFERENCE: MBHB01-662A
;  CURRENT APPLICATION NUMBER: PCT/US02/37235
;  CURRENT FILING DATE:  2003-06-16
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
;   LENGTH: 4593
;   TYPE: DNA
;   ORGANISM: Actinobacillus actinomycetemcomitans
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(4593)
PCT-US02-37235-43

Alignment Scores:
Pred. No.:              3.39e-06        Length:         4593
Score:                  131.50          Matches:        179
Percent Similarity:     33.33%          Conservative:   120
Best Local Similarity:  19.96%          Mismatches:     323
Query Match:            3.33%           Indels:         275
DB:                     1               Gaps:           47

US-09-494-297-2 (1-757) x PCT-US02-37235-43 (1-4593)

Qy         39 AlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSerSerThr 58
              |||   :::|||:::                   :::   |||         |||||||||
Db       1621 GCCAATATCACCGCGACAACCAACGGTTCCGTCATTTTAGGA------AATTCCTCCACC 1674

Qy         59 ProAsnAlaIleAsnProAspSerSer-----------------SerGluTyrArgTrp 72
                        :::|||  |||:::                 :::   |||  :::
Db       1675 ACGGAAGGTTCACATCCTGTTTCAAATGTTAGCAGTGCGACTGTTAACGGATATACCTAC 1734

Qy         73 TyrGlyTyrGluSerTyrValArgGlyHisProTyrTyrLysGlnPheArgValAlaHis 92
                 |||:::         |||:::         ::::::
Db       1735 TCAGGTTTTACCGGCACGGTAAAAGAGTCGGGACATTTTGTGAGCATT------------ 1782

Qy         93 AspLeuArgValAsnLeuGluGlySerArgSerTyrGlnValTyrCysPheAsnLeuLys 112
                                 ||||||:::      :::           |||:::
Db       1783 ---------------------GGTTCAAAAGGCAATGAGCGTCAAATTAAAAATGTG--- 1818

Qy        113 LysAlaProProLeuGlySerAspSerSerValLysLysTrpTyrLysLysHisAspGly 132
                    |||     :::   ::::::|||:::                        |||
Db       1819 GCAGCAGGTAATGTTGCGGCAAACTCAACC----------------------GATGCC 1854

Qy        133 IleSerThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsn 152
                   ::::::         :::   :::|||::::::   |||:::         |||
Db       1855 GTTAATGGCTCT---CAATTATTTGCTGTCGCCAGTCGTGTA---------GAACAAGGT 1902

Qy        153 GlnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGlu 172
                 ::::::  :::   :::  ||||||      ||||||
Db       1903 TGGCAAATCACTTCCGGCGTAGAAAATGGTGGTACTCAAAATGGCGCAGCCTCAACAGCA 1962

Qy        173 GlyLeuGluProLeuAsnAlaIleArgVal---------ThrGlnGluAlaValTrpTyr 189
                    :::::::|||   |||  :::::::::                  ||||||
Db       1963 ACAATCAAACCGAGTAACCAAGTGAAGCTACTGGCAGGAAAGAATTTAGCAGTCAAACAA 2022

Qy        190 TyrSerAspAsnAlaProIleSerAsnProAspGlu---SerPheLysArgGluSerGlu 208
                       |||         |||      :::      :::|||         :::
Db       2023 AACGGCACTAACTTCACCTTCTCAACCCAAGAAAATGTCACGTTCACTAATGTTACGACC 2082

Qy        209 SerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGln------ 226
                 :::|||   :::|||         ::::::         :::::::::
Db       2083 CAAGATCTAACTGCAACAGGCAACACCACTGTTAAGAACTTCAGCGTTCAAAATGGCGGA 2142
```

```
Qy       227 ------LeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspPhe 244
Db      2143 ACCATCAATATGGGAAATAATCGCATTACCGGTGTCGCTGAAGGCACTCAAGATGAC--- 2199

Qy       245 GlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyrAsn---LysGlyTyrGln 263
Db      2200 --------------------------------GACGCGGTTAACTTTAAACAATTAAAA 2226

Qy       264 AsnLeuLeuSerGlyGly------------LeuValProThrLysProProThrProGly 279
Db      2227 AGCCTTCTTGGTGGCTCCGCATCAACGGAAATTGTTGAGAAAAAAGCAGCTCAAGCCGGA 2286

Qy       280 AspProProMetProPro---------AsnGlnProGlnThrThrSerValLeuIleArg 296
Db      2287 GATGAAAACCTGGCGGATATTAGCGTAGCAAATGGTAAAAACGCCGGCGATATGGGTGCG 2346

Qy       297 LysTyrAlaIleGlyAspTyrSerLysLeuLeuGluGlyAla---------ThrLeuGln 313
Db      2347 AAATACGAAGTATCTGTATCCAAAAAAGCCGTACAAAGTGCCGCAAAAGAAGCGGTTAAA 2406

Qy       314 LeuThrGlyAsp---------AsnValAsnSerPheGln---------------------- 323
Db      2407 GTGACAGGTTCGGCACCGATTAATGTAAACAAAACAGATGTAAATGGCGTTGATACTTAT 2466

Qy       324 AlaArgValPheSerSerAsnAspIleGlyGluArgIleGluLeuSer------------ 339
Db      2467 GCCGTAACCTTTAATGGCACAGAAGCGGCGAAATCTATCCCATTAACTTATAAAGCTAAC 2526

Qy       340 ---------AspGlyThrTyrThrLeuThrGlu---LeuAsnSerProAlaGlyTyrSer 355
Db      2527 GGTAGCGGTGATAAAACCGTCATGTTGGATAAAGGATTAAACTTTACCAATGGTATGATG 2586

Qy       356 IleAlaGluProIle-------------------------------------ThrPhe 362
Db      2587 ACAACCGCTTCCGTGGCAAATGACGGTGTGGTGAAATATGACGTCAATTTATCCACCATT 2646

Qy       363 LysValGluAlaGlyLysValTyrThrIle---------------------------- 372
Db      2647 AAAGTAGAAGATGGCAAGGCTGCCGTAGCCGGTACACCGGGCACAAATGGCGCCAACGGC 2706

Qy       373 IleAspGlyLysGlnIleGluAsnProAsnLysGluIleValGluProTyrSerValGlu 392
Db      2707 ACTGATGGCAAAGATGGCGTAGCGACGGTTAAAAATGTGGTAGAGGCGTTAAATAATGCC 2766

Qy       393 AlaTyr-----------------AsnAspPheGluGluPheSer--------------- 401
Db      2767 GCATGGACAATAACTGCCTCTAAATCTGACGGCGAAGTCGTCAGCAATGCATCTAATTCC 2826

Qy       402 ----------------------------------------ValLeuThrThrGlnAsn 407
Db      2827 GTTAAAAATGGGGATACGGTGACTTATGATGCCGGCAAAAACATCAAAATTACTCAAAGA 2886

Qy       408 TyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValValTyrCysPhe 427
Db      2887 GATAAAAAATTCTCTTTTGCCACCAAAGATAATGTTGAATTTACTTCTGTGACCACGGGC 2946

Qy       428 AsnAlaAspLeuLys---SerProProAspSerGluAspGlyGlyLysThrMetThrPro 446
Db      2947 AATACCAAATTAACCGGTAATGGTGTAGAAATCACCAACGGCCCTAAACTTACCCAATCA 3006

Qy       447 AspPheThrThrGlyGluValLysTyrThrHisIleAla--------------------- 459
Db      3007 GGTGTGGATGCAGGCGGTAAGAAAATCACCAATGTAGCAGATGGCGTTATTGCAGCTAAC 3066

Qy       460 -----------------GlyArgAspLeuPheLysTyrThrValLysProArg------ 471
Db      3067 AGCAAAGATGCCGTGAATGGCGGTCAATTATTCGCTGAAACTGCAAAAGCCAAAACTACG 3126

Qy       472 ----------------------------------AspThrAspProAspThrPheLeu 479
Db      3127 GTTGAGAAAGGTGATGATAATATTCAAATCACATCAGAAACTGCAACGGACGGACATATT 3186

Qy       480 LysHis---------IleLysLysValIleGluLysGlyTyrArgGluLysGlyGlnAla 496
Db      3187 AACTATAAAGTGGCATTAAATCCTAGCTTGACCGTCGGACCAAGAACAAATGGTCACCCG 3246

Qy       497 IleGlu--------------------TyrSerGlyLeuThrGluThrGlnLeu------ 507
Db      3247 ATCACCATTGATGGTAATAACGGCTATATTACCGGTTTAACCAATACAAGCTGGACGGGC 3306

Qy       508 ---------------ArgAlaAlaThr------GlnLeuAlaIleTyr------TyrPhe 518
Db      3307 GCGCCAACAACCGGTCGTGCAGCAACGGAAGATCAATTATCTATAGTCGATAAAAAATTC 3366

Qy       519 ThrAspSerAlaGluLeu------------------------------------------ 524
Db      3367 GATAATAAGGTTTCTTTAGGCGGTGACAACGGTAGTACCACAGAGAAATCCTTGTCTCAC 3426

Qy       525 --------------------------------AspLysAspLysLeuLysAspTyrHis 533
Db      3427 AACGGCGGAATCAAATTTAATATCAAAGGCGGAGACAGCCAAAAATATGTGACGACATCA 3486

Qy       534 GlyPheGlyAspMetAsnAspSerThrLeuAlaValAla---------LysIleLeuVal 550
Db      3487 GGATCCGGCGAT------GATGTCACGGTGGATCTTGCCCAAACCACAAAAAATAAGATC 3540

Qy       551 GluTyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsn 570
Db      3541 GACAATGCGGCAGATAAAGATCTCGCCAACATTACCGAT-----------------AAT 3582

Qy       571 AsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAspLeuValAspIle 590
Db      3583 GGTAAAAAAGTTATTACCGCTTTAGGCGCT--------------------------GTA 3615

Qy       591 IleArgMetGluAspLysLys---GluValIleProValThrHisAsnLeuThrLeuArg 609
Db      3616 GTGAAAGCGGCTGATTCTACGATTACGGTAACTGACGAAACCGATAATACGACAGGACAA 3675

Qy       610 LysThrVal------------------------------------------------- 612
Db      3676 AAAACCTACAAAATCAAAGCCAATATTCCAACACCGGAAAAAACAGCAATGGCTCCCGGC 3735

Qy       613 ------ThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeuLys 630
Db      3736 AACAATACAACCATTGAAGGTGATGGCTCAGCCGCCAATCCGTTTAAAGTGAATCTGAAA 3795

Qy       631 AsnAsn------------LysGlnGluLeuLeuSerGlnThrValLysThrAspLysThr 646
Db      3796 GATGATTTAGCGCTAGGTCAAAAAGACGCTAACGGCGTAACCGGTAAAGATTCTTCCATT 3855

Qy       647 AsnLeuGluPheLysAspGlyLys---AlaThrIleAsnLeuLysHisGlyGluSerLeu 665
Db      3856 AAAGTGAACGGCAAAGATGGCTCCGGTGTGGCGATTAACGGTAAAGACGGT---TCCATT 3912

Qy       666 ThrLeuGlnGlyLeu------------------------------------ProGlu 672
Db      3913 GCATTAAATGGCAAAGACGGTGCGAATCCTGTCACCATCAAAACGGCGCAAGGTCCTGCC 3972

Qy       673 GlyTyrSerTyrLeuValLysGluThrAspSerGluGlyTyrLysValLysValAsnSer 692
Db      3973 GGT------------GTGAATGAAACCAATCCCAAAGAC---CGTTTAATGGTGAATAAC 4017

Qy       693 GlnGluValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGluThrLeuAla 712
Db      4018 GACGCTGTTGCAACCCTT---------AAAGACGGCTTA-----------AAATTCGCC 4056

Qy       713 PheGluAsnAsnLysGluProValValProThrGlyValAspGlnLysIle 729
Db      4057 GGAGATAACAGCACCGAAGTCATCACTAAAACC---TTAAATCAAAAACTG 4104
```

RESULT 7
PCT-US03-22113-28
; Sequence 28, Application PC/TUS0322113
; GENERAL INFORMATION:
; APPLICANT: Seattle Genetics, Inc.

```
;  TITLE OF INVENTION: SGA-72M, A CANCER ASSOCIATED ANTIGEN AND USES THEREOF
;  FILE REFERENCE: 9632-061-228
;  CURRENT APPLICATION NUMBER: PCT/US03/22113
;  CURRENT FILING DATE:  2003-07-11
;  PRIOR APPLICATION NUMBER: 60/395,752
;  PRIOR FILING DATE: 2002-07-11
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
;   LENGTH: 4371
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US03-22113-28

Alignment Scores:
Pred. No.:              3.62e-06     Length:          4371
Score:                  131.00       Matches:         160
Percent Similarity:     35.48%       Conservative:    126
Best Local Similarity:  19.85%       Mismatches:      252
Query Match:            3.32%        Indels:          268
DB:                     1            Gaps:            45

US-09-494-297-2 (1-757) x PCT-US03-22113-28 (1-4371)

Qy         54 ValGluSerSerThrProAsn--------------------AlaIleAsnProAspSer 66
Db       1396 GTGGCAGACAGTTTGCCTTCTAGAAGAAACATTACTTTACCAGCACTGCAACCTCCCTCA 1455

Qy         67 SerSerGluTyrArgTrpTyrGlyTyrGluSerTyrVal---------ArgGlyHisPro 83
Db       1456 AAT---------------GTCGGGAGTGAACGACATGCTCCATTGGAGAAAGACAGACCT 1500

Qy         84 TyrTyrLysGln------------PheArgValAlaHisAspLeuArgValAsnLeuGlu 99
Db       1501 CTAGTTCGTGAATCAAATGCCAACTTTAAAGTTATG---TCCCTAAAAGAAAGAATGGAT 1557

Qy        100 GlySerArgSerTyrGlnValTyr------------CysPheAsnLeuLysLysAlaPhe 115
Db       1558 GAACCCAATGCAGAACAGGTCTATAATCCCTCTCAGTTTGAGAATTTGAGAAAGTTTTGG 1617

Qy        116 ProLeuGlySerAspSerSerValLysLysTrpTyrLys---------------------- 128
Db       1618 GACTTAGAAGCTAATTCAAACAGTAAGGATAATGACAAGAATATTACCACCACAAGCCAA 1677

Qy        129 ---------------------------LysHis-----------------------Asp 131
Db       1678 AAAAATTCTGCACCTTTTAATAGGCAGAAACACAAGGAATTCAGCGACATTAAATTATCA 1737

Qy        132 GlyIleSerThrLysPheGluAspTyrAlaMetSerPro---ArgIleThrGlyAspGlu 150
Db       1738 GGTAAAAATACCCATGAAGCAGAGGTGCTTCTAAGCCCAAAAAAAGTTATGGCAAGAGAG 1797

Qy        151 LeuAsnGlnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIle 170
Db       1798 GAAATGGAGAAATTA----------------------------AATTCAAAGGGCATA 1827

Qy        171 MetGluGlyLeuGlu--------------ProLeuAsnAlaIleArgValThrGlnGlu 185
Db       1828 CTCCAGGTGCTACCAGATGAAATCACATTTCCTTTGAGTCCACTTAGA------------ 1875

Qy        186 AlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerPheLysArg 205
Db       1876 ---------AAGTATACTTATCAGTTGCCA---------GGAAATGAGTCATCAAAGGAA 1917

Qy        206 GluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLys 225
Db       1918 AATGTGGAAAAGAAT------------------------------------------- 1932

Qy        226 GlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAsp--------- 242
Db       1933 ---------ACGGAAGGGATTGTTACTCCAGTGTTTAAGGAAGAAAAGGATTACTCAGAA 1983

Qy        243 ---AspPheGlnLeuSerIlePheGlu------------SerGluAspLysGlyAspLys 257

Db       1984 CAAGAGATTCAAGAATCCATAATAAAAACCAATGTTTTGTCTAAAGACTGCAAAGACACT 2043

Qy        258 TyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValProThrLysProProThr 277
Db       2044 TTTAATGACAGCTTGCAGAAACTGCTTTCAGAAACCTCAACACCAGCAATTCAACCCTCT 2103

Qy        278 ProGly-----------------------AspProProMetProProAsnGln------ 287
Db       2104 GGTGGAAAAGTTCATGGAAAACAAGTGCTTGAACCAAGTGTTTCTGAAAATAGGACATGG 2163

Qy        288 ProGlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeu 307
Db       2164 CCTCAAAAAACAGAT--------------------TTTGGTGATACTGAGGAAGAAGTC 2202

Qy        308 GluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPhe 327
Db       2203 AAAGGACCTGAG---AAGATCATTAATGAGCATGTTGAC-------------------- 2238

Qy        328 SerSerAsnAspIleGlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGlu 347
Db       2239 ---AAAACAGTAGTTCATCCAAAGGTTAAACGGAACTCTTTGACTGCTAGTCTAGACAAA 2295

Qy        348 Leu-----------------------AsnSerProAlaGlyTyrSerIleAlaGluPro 359
Db       2296 CTCCTGAAGGAAGCAACTGGAACTTCACCCTCTCCCTTGCAAGCCAAGTTGGCGCCCGTT 2355

Qy        360 IleThr---------PheLysValGluAlaGlyLysValTyrThrIleIleAspGlyLys 376
Db       2356 ATCACTGGAACCAACTCTAAGCTGGAAGAGGGGAGATTTTTT-----------GGAAAA 2403

Qy        377 GlnIleGluAsnProAsn-----------------LysGluIleValGluProTyrSer 390
Db       2404 GGGATAGAACAGAGTCACAATACTTCAGCTGATAAGAGAGAAATACTAGCTCCTTTTCCA 2463

Qy        391 ValGluAlaTyrAsnAspPheGluGluPheSer--------------------------- 401
Db       2464 GTGAGAGAT------------GAAACTTTTGGAAATACAGCTCTCCTCAAGAAAGCTGAA 2511

Qy        402 ------------ValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLys------ 415
Db       2512 AGTGGTGAGTGCCAGCTAAGCACACAGAATTTGATTCAGGTGGCTGCAGAAGATTCTCAT 2571

Qy        416 -----------------------AsnLysAsnGlySerSerGlnValValTyrCysPhe 427
Db       2572 CCATTGGATCCAACTTCCCAGCTTTCCAGAAAGGGTTCTTTT----------------- 2613

Qy        428 AsnAlaAspLeuLysSerProProAsp--------------------------------- 436
Db       2614 ---GGGGATGTGGCCAGCCCTCCCCAAGATATGCTTTTTCCCCAGGGTGCTCATCTTGTT 2670

Qy        437 ----------------------------------SerGluAspGlyGlyLysThrMet 444
Db       2671 CCCCAGGCTAGGGTACACCCTTCTCAAATGGAAATTTCGGAGACTGTAGAGAAAGTCATT 2730

Qy        445 ThrPro------------------AspPheThrThr-----------------GlyGlu 452
Db       2731 CTTCCACCCAGACCTGTATTGAATGATGTAAGTGCTGCATTACAGAAGCTGTGTGGAGAA 2790

Qy        453 ValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAsp 472
Db       2791 GTATGGTTAAGTTATCCAGCTGGAAGGGAA--------------GTAGGTCCTGGAGAA 2835

Qy        473 ThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLysGlyTyrArgGlu 492
Db       2836 GTGAACCCAGAA---TTTCCTGAAGCAGTACAGCCAGTATGT----------------- 2874

Qy        493 LysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGln 512
Db       2875 ----------------------------------AGCCCCCTAAATCCTCCAGGAGTG 2898

Qy        513 LeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyr 532
```

```
Db       2899 ATATCACCATGGGCTACGATGGACACCATAGTTCCAGACAGG---------AAGGATTTT 2949

Qy        533 HisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyr 552
              :::           :::   |||   |||      |||         |||
Db       2950 TATTCCTCCAATGTAGTTCCTGATAAAACTCATGAAGTTGGATCTTATTTA--------- 3000

Qy        553 AlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsn 572
              |||         :::|||         |||                         :::
Db       3001 GCTGCCCAAATGTCTCCATCAGACCAGACG----------------------CTTAGC 3036

Qy        573 LysTyrGlnSerLeuIleGlyThr------GlnTrpHisProGluAspLeuValAspIle 590
                :::   |||::::::           :::      |||:::::::::   :::|||
Db       3037 TCATTTGCTTCCATTGTTGCTCAATATGGCAAAGGCCTCCCTCAGGAAGTGGAAGAAATT 3096

Qy        591 IleArgMetGluAspLysLysGluValIleProValThrHisAsnLeuThrLeuArgLys 610
              :::|||         :::      |||   |||   :::      |||
Db       3097 GTGAGG---------GAAACAATTGTTCAACCCAAATCAGAGTTCCTCGAATTCAGTGCT 3147

Qy        611 ThrValThrGlyLeuAlaGlyAspArgThrLysAspPhe------HisPheGluIleGlu 628
                :::      |||      :::   |||:::   |||         :::|||   :::
Db       3148 GGCTTAGAAAAACTACTGAAGGAAGAAACTGAAACCTTCCCCTCAAAATATGAAAGTGAT 3207

Qy        629 LeuLysAsn---AsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsn 647
                |||   :::      :::|||:::      |||   :::      :::
Db       3208 ACAGGGAATCTTTCTCCATCAAAGTTAATAGGTAGTACAGAGGAGCCCAGGCGAGCCACT 3267

Qy        648 LeuGluPhe------LysAspGlyLysAlaThrIleAsnLeuLysHisGlyGluSerLeu 665
                |||         ::::::   |||   |||:::                     :::
Db       3268 TCTGAATGCCATCCTGAGGAATTAAAAGAAACAGTAGAAAAGGCCGAGGCTCCATTAATA 3327

Qy        666 ThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGlu---ThrAspSerGlu 684
              |||                  |||:::      |||:::||||||   |||::::::
Db       3328 ACTGAGAGTGCTTTTGATGCTGGTTTTGAGAAACTTCTTAAAGAAATAACTGAAGCTCCT 3387

Qy        685 GlyTyrLysValLysValAsnSerGlnGluValAlaAsnAlaThrValSerLysThrGly 704
                |||:::   :::|||:::   :::|||            |||      |||
Db       3388 CCTTATCAGCCCCAGGTGTCAGTGAGAGAA---------GAAACTCACGAGAAGGAGTCC 3438

Qy        705 IleThrSerAspGluThr 710
                |||:::::::|||
Db       3439 TCACAGTCAGAGCAGACC 3456

RESULT 8
US-10-450-826-5
; Sequence 5, Application US/10450826
; GENERAL INFORMATION:
;  APPLICANT: Ji, Darren
;  APPLICANT:  Axelrod, Douglas W.
;  APPLICANT:  Cook, Jonathon S.
;  APPLICANT:  Jaiswal, Neelam
;  APPLICANT:  Eistein, Richard
;  APPLICANT:  Houghton, Adam
;  APPLICANT:  Mertz, Lawrence
;  TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiati
;  FILE REFERENCE: 044921-5039-WO
;  CURRENT APPLICATION NUMBER: US/10/450,826
;  CURRENT FILING DATE:  2003-06-18
;  PRIOR APPLICATION NUMBER: US 60/255,882
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: US 60/285,691
;  PRIOR FILING DATE: 2001-04-24
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 5043
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. AB037755
US-10-450-826-5

Alignment Scores:
Pred. No.:              4.74e-06        Length:         5043

Score:                  131.00          Matches:        151
Percent Similarity:     36.79%          Conservative:   101
Best Local Similarity:  22.04%          Mismatches:     263
Query Match:            3.32%           Indels:         171
DB:                     6               Gaps:           36

US-09-494-297-2 (1-757) x US-10-450-826-5 (1-5043)

Qy        124 LysLysTrp---TyrLysLysHisAspGlyIleSerThrLysPheGluAspTyr------ 140
              |||||||||      ||||||            :::|||   ::::::   |||
Db       1049 AAGAAGTGGAACTCCAAAAAAACGCAAAGCTCCACCACCTCCTATCAGTCCTACCCAGTT 1108

Qy        141 ------AlaMet-SerProArg---IleThrGlyAspGluLeuAsnGlnLysLeuArgAl 157
                    ::: |||||||||   ||||||         |||:::   |||      ::
Db       1109 GAGTGATGTCTCTTCCCCAAGATCAATAACTTCGACTCCACTATCGGGAAAG---GAATC 1165

Qy        157 aValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLe 177
              :|||   :::          |||      |||                         ::
Db       1166 GGTATTTTTGCTGAACCACCCTTCAAGGCTGAG----------------------AT 1201

Qy        177 uAsnAlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSe 197
              :::::::||||||      ::::::   :::         |||||||::         ::
Db       1202 CAGTTCTATACGAGAAAACAAAGACAGACTA---------AGTGACAGTACT------AC 1246

Qy        197 rAsnProAspGluSerPheLysArgGluSerGluSer---------AsnLeuValSerTh 214
              :    |||                    ||||||:::         :::|||:::|||
Db       1247 AGGTGCTGATAGCTTATTGGATATAAGTTCTGAAGCTGACCAACAAGATCTTCTCTCTCT 1306

Qy        214 rSerGlnLeuSerLeuMetArgGlnAlaLeu------LysGlnLeuIleAspProAsnLe 232
                  |||      :::             |||      |||:::|||   |||      ||
Db       1307 ATTGCAAGCAAAAGTTGCTTCCCTTACCTTACACAATAAGGAGTTACAAGAT---AAATT 1363

Qy        232 uAlaThrLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSer-- 251
              |      |||   ||||||:::         |||                :::   |||
Db       1364 ACAGGCCAAATCACCCAAGGAGGCGGAAGCAGACCTAAGCTTTGACTCATACCATTCCAC 1423

Qy        252 ----GluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLe 270
                  |||   |||            |||
Db       1424 CCAAACTGACTTGGGCCCATCCCTGGGAAAA---------------------------- 1454

Qy        270 uValProThrLysProProThrProGlyAspProProMetProProAsnGlnProGlnTh 290
                                  ||||||:::         |||||||:::         ::
Db       1455 ----------------------CCTGGTGAA---ACCTCTCCCCCAGACTCCAAATCATC 1489

Qy        290 rThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuGluGlyAl 310
              :   ||||||||||||      :::::::::|||       |||
Db       1490 TCCATCTGTCTTAATA----:-CATTCTTTAGGTAAA---TCCACTACTGACAATGATGT 1540

Qy        310 aThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAs 330
              :::|||         :::   :::          |||   |||:::   ||||||
Db       1541 CAGAATTCAGCAACTGCAAGAGATTTTGCAAGATCTACAGAAGAGATTAGAGAGCTCTGA 1600

Qy        330 nAspIleGlyGluArg-----------IleGluLeuSerAspGlyThrTyrThrLeuTh 346
                    ||||||            :::||||||                     |||
Db       1601 A------GCAGAGAGAAAACAGCTACAGGTCGAACTCCAATCCCGAAGGGCAGAACTGGT 1654

Qy        346 rGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAl 366
                  ||||||:::                  :::      ::::::   |||::::::
Db       1655 ATGCTTAAACAACACTGAGATTTCAGAGAACAGCTCTGACCTCAGCCAGAAACTTAAAGA 1714

Qy        366 aGlyLysValTyrThrIleIleAspGlyLysGlnIleGluAsnProAsnLysGlu----- 384
              :::                        |||::::::   :::      |||:::
Db       1715 AACTCAGAGCAAATACGAGGAGGCTATGAAAGAAGTCCTTAGTGTGCAGAAGCAGATGAA 1774

Qy        385 -------IleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPheSerVa 402
                    :::|||   |||   |||::::::   |||:::   |||   |||      ||
Db       1775 ACTCGGTCTTGTCTCACCTGAAAGCATGGATAATTATTCACATTTCCACGAGCTGAGGGT 1834

Qy        402 lLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGl 422
              |          |||                           |||   ||||||:::::
Db       1835 CACGGAAGAGGA-AATAAATGTGCT-----------------AAAGCAGGATCTGCAGA 1875

Qy        422 nValValTyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAsp---GlyGl 441
```

```
Db       1876 A---------TGCATTAGAAGAAAGTGAAAGAAATAAAGAGAAAGTGAGAGAGTTAGAGG 1926

Qy        441 yLysThrMetThrProAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyAr 461
Db       1927 AAAAACT-------------------------------------------------GGTAG 1938

Qy        461 gAspLeuPheLysTyrThr-ValLysProArgAspThrAspProAspThrPheLeuLysH 481
Db       1939 AGAGGGAGAAAGGTACAGTGATTAAGCCACCTGTGGAAGAGTACGAGGAAATGAAAAGTT 1998

Qy        481 isIleLysLysValIleGluLysGlyTyrArgGluLysGlyGlnAlaIle---------- 497
Db       1999 CATATTGCTCTGTTATTGAGAATATGAATAAGGAGAAAGCATTTTTGTTTGAGAAATACC 2058

Qy        498 -------------GluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnL 513
Db       2059 AAGAAGCCCAAGAAGAAATCATGAAATTAAAAGACACACTAAAAAGTCAGATGACACAGG 2118

Qy        513 euAlaIleTyrTyrPheThrAspSerAla---------------------------- 522
Db       2119 AAGCC------------AGTGATGAAGCTGAGGACATGAAAGAAGCCATGAATAGGATGA 2166

Qy        523 -----GluLeuAspLysAsp-------------------------------------L 528
Db       2167 TAGATGAACTCAATAAACAGGTGAGCGAGCTGTCACAGCTGTACAAAGAAGCCCAGGCTG 2226

Qy        528 ysLeuLysAspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysI 548
Db       2227 AGCTGGAGGATTACAGGAAGAGGAAATCTCTAGAGGATGTCACA---------------- 2270

Qy        548 leLeuValGluTyr---------AlaGlnAspSerAsnProProGlnLeuThrAspLeu- 564
Db       2271 -----GCTGAATATATCCATAAAGCAGAGCATGAGAAACTGATGCAATTGACAAACGTGT 2325

Qy        565 ----------------AspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIleG 579
Db       2326 CCAGGGCTAAAGCAGAAGATGCACTGTCTGAAATGAAGTCTCAGTATTCAAAAGTGTTGA 2385

Qy        579 lyThrGlnTrpHisProGluAspLeuValAspIleIleArgMetGluAspLysLysGluV 599
Db       2386 ATGAGTTGACCCAGCTCAAACAACTGGTGGAT-----------GCACAAAAAGAGAACT 2433

Qy        599 alIleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspA 619
Db       2434 CTGTCTCTATCACAGAACATTTGCAAGTGATAACCACGCTG----------------C 2475

Qy        619 rgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerG 639
Db       2476 GGACTGCAGCAAAAGAGATGGAAGAAAAAATAAGCAATCTTAAGGAACACCTTGCAAGCA 2535

Qy        639 lnThrValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnL 659
Db       2536 AGGAAGTGGAAGTAGCAAAGCTGGAGAAACAACTCTTAGAAGAGAAAGCT---------- 2585

Qy        659 euLysHisGlyGluSerLeuThrLeuGlnGlyLeuPro---GluGlyTyrSerTyrLeuV 678
Db       2586 -------------GCTATGACTGATGCAATGGTACCTCGGTCTTCCTATGAAAAACTCC 2631

Qy        678 alLysGluThrAspSerGluGlyTyrLysValLysValAsnSerGlnGluValAlaAsnA 698
Db       2632 AGTCATCCTTAGAGAGTGAA---------GTGAGTGTGTTGGCATCGAAATTAAAGGAAT 2682

Qy        698 laThrValSerLysThrGlyIleThrSerAsp-----------------GluThrLeuA 712
Db       2683 CTGTGAAAGAGAAAGAGAAGGTCCATTCAGAGGTTGTCCAGATTAGAAGTGAGGTCTCAC 2742

Qy        712 laPheGluAsnAsnLysGluProVal------ValProThrGlyValAspGlnLysIleA 730
Db       2743 AGGTGAAAAGAGAAAAGGAAAATATTCAGACTCTCTTGAAATCCAAAGAGCAAGAAGTAA 2802

Qy        730 snGlyTyrLeu 733
Db       2803 ATGAACTTCTG 2813
```

RESULT 9
US-60-490-890-1650
; Sequence 1650, Application US/60490890
; GENERAL INFORMATION:
; APPLICANT: Li, Martha
; APPLICANT: Rupnow, Brent A.
; APPLICANT: Webster, Kevin R.
; APPLICANT: Jackson, Donald
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
; FILE REFERENCE: D0310 PSP
; CURRENT APPLICATION NUMBER: US/60/490,890
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2779
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1650
; LENGTH: 3371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-490-890-1650

Alignment Scores:

Pred. No.:	3.06e-06	Length:	3371
Score:	130.00	Matches:	118
Percent Similarity:	36.94%	Conservative:	104
Best Local Similarity:	19.63%	Mismatches:	233
Query Match:	3.30%	Indels:	148
DB:	7	Gaps:	30

US-09-494-297-2 (1-757) x US-60-490-890-1650 (1-3371)

```
Qy        143 SerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMetTyrAsnGly 162
Db        165 TCCCCCAAGCCTCTGTGTAATCCTCTGAGGAGAAAAGCCCATAGCTTGAAAGTTCGGGGG 224

Qy        163 HisProGlnAsnAlaAsnGlyIleMet-----------GluGlyLeuGluProLeuAsn 178
Db        225 CAT--------------TTTGTTGTGTTCTGTAGGAGAGAGGGGGAGGACCCTGTTCGG 269

Qy        179 AlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsn 198
Db        270 GTAGTTTGGCCGGAC----------TGGTACTGG----------CCGTTGGAAAAC 305

Qy        199 ProAspGluSerPheLysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSer 218
Db        306 CCGAAGTA-CATTTCCGT--------------------GTGGAACTTTTGCAGATATAT 343

Qy        219 LeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLys 238
Db        344 ATTTTTAGATT-TTTAAATACCAGATAAAAAATATATGCCTTCTATATATCTCCTGGCGA 402

Qy        239 GlnValProAspAspPheGlnLeuSerIlePheGluSerGluAspLysGlyAsp------ 256
Db        403 CCTGCCCCTGACAGCGCGATGTACAATACGGTGTGGAGTATGGACCGCGATGACGCAGAC 462

Qy        257 ------LysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValProThrLys 274
Db        463 TGGAGGGAGGTGATGATGCCCTATTCGACAGAACTGATATTTTATATTGAAATGGATCCT 522

Qy        275 ProProThrProGlyAspProProMetPro---------------ProAsnGlnProGln 289
Db        523 CCAGCTCTTCCACCAAAGCCACCTAAGCCAATGACTTCAGCAGTTCCAAATGGAATGAAG 582

Qy        290 ThrThrSerValLeuIleArg------LysTyrAlaIleGlyAspTyrSerLysLeuLeu 307
Db        583 GACAGTTCTGTTTCTCTTCAGGATGCAGAATGGTACTGGGGGGATATTTCAAGG------ 636

Qy        308 GluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPhe 327
Db        637 --------------GAGGAGGTAAATGACAAATTGCGGGATATGCCAGATGGGACCTTC 681
```

```
Qy       328 SerSerAsnAspIleGlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThr--- 346
Db       682 TTGGTCCGAGATGCCTCAACAAAAATGCAG---------GGAGATTATACTTTGACTTTG 732

Qy       347 ----------------------------GluLeuAsnSerProAlaGlyTyrSerIle 356
Db       733 CGGAAGGGAGGCAATAATAAGTTAATAAAGATCTATCACCGGGATGGTAAATATGGCTTT 792

Qy       357 AlaGluProIleThrPheLysValGluAlaGlyLysValTyrThrIleIleAspGlyLys 376
Db       793 TCTGATCCTCTGACATTT-----------AATTCCGTGGTGGAGCTCATTAACCACTAT 840

Qy       377 GlnIleGlu--------------AsnProAsnLysGluIleValGluProTyrSerVal 391
Db       841 CACCATGAATCTCTTGCTCAGTACAATCCCAAACTTGATGTGAAGCTGATGTACCCAGTG 900

Qy       392 GluAlaTyrAsnAsp---------PheGluGluPheSerValLeuThrThrGlnAsnTyr 408
Db       901 TCCAGATACCAACAGGATCAGTTGGTAAAAGAAGATAATATTGATGCAGTAGGTAAAAAA 960

Qy       409 AlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValValTyrCysPheAsn 428
Db       961 CTGCAAGAATACCACTCTCAGTATCAGGAGAAGAGTAAAGAGTATGATAGGCTGTATGAA 1020

Qy       429 AlaAspLeuLysSerProProAspSerGluAspGlyGlyLysThrMetThrProAspPhe 448
Db      1021 GAATATACTAGAACATCCCAGGAAATA------------------------------- 1047

Qy       449 ThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThrVal 468
Db      1048 ---------CAGATGAAGAGGACTGCAATA---------GAAGCTTTTAATGAAACAATT 1089

Qy       469 LysProArgAspThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLys 488
Db      1090 AAAATATTTGAAGAGCAGTGTCACACACAAGAACAACATAGCAAAGAATATATTGAGCGA 1149

Qy       489 GlyTyrArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArg 508
Db      1150 ---TTTCGCAGAGAGGGGAATGAAAAGGAGATTGAACGAATTATG--------------- 1191

Qy       509 AlaAlaThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLys 528
Db      1192 ----------------------------------------------ATGAATTATGATAAA 1206

Qy       529 LeuLysAspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIle 548
Db      1207 TTGAAATCA------CGTCTGGGTGAGATTCATGATAGCAAAATGCGTCTAGAGCAGGAT 1260

Qy       549 LeuValGluTyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPhePheIle 568
Db      1261 TTGAAGAAACAAGCTTTGGACAACCGA--------------GAAATAGAT--------- 1296

Qy       569 ProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAspLeuVal 588
Db      1297 ---------AAAAAAATGAATAGTATC-----------------AAACCTGACCTGATC 1329

Qy       589 AspIleIleArgMetGluAspLysLysGluValIleProValThrHisAsnLeuThrLeu 608
Db      1330 CAGCTGCGAAAGATCCGAGAT---CAACACCTTGTATGGCTCAATCACAAA--------- 1377

Qy       609 ArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGlu 628
Db      1378 ----------------------GGAGTGAGACAGAAACGCCTGAATGTCTGGCTGGGA 1413

Qy       629 LeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeu 648
Db      1414 ATTAAGAATGAGGATGCTGAT---GAGAACTATTTTATCAATGAGGAAGATGAAAACCTG 1470

Qy       649 GluPheLysAspGlyLysAla------------ThrIleAsnLeuLysHisGlyGluSer 664
Db      1471 CCCCATTATGATGAGAAAACCTGGTTTGTTGAGGATATCAATCGAGTACAAGCAGAGGAC 1530

Qy       665 LeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAspSerGlu 684
Db      1531 TTG---CTTTATGGGAAACCTGATGGT---GCATTCTTAATTCGTGAGAGTAGCAAGAAA 1584

Qy       685 Gly---TyrLysValLysValAsnSerGln---GluValAlaAsnAlaThrValSerLys 702
Db      1585 GGATGCTATGCTTGCTCTGTGGTGGCCGATGGGGAAGTGAAGCACTGTGTGATCTACAGC 1644

Qy       703 Thr 703
Db      1645 ACT 1647
```

RESULT 10
US-10-623-500-12/c
; Sequence 12, Application US/10623500
; GENERAL INFORMATION:
; APPLICANT: Bayer BioScience N.V.
; APPLICANT: Greet, Vanderkimpen
; APPLICANT: Gerben, Van Eldik
; APPLICANT: Frank, Meulewaeter
; TITLE OF INVENTION: Corn root preferential promoters and uses thereof
; FILE REFERENCE: 021565-119
; CURRENT APPLICATION NUMBER: US/10/623,500
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 60/399383
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 8514
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pTWV011
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (52)..(1)
; OTHER INFORMATION: LB= left T-DNA border
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (318)..(58)
; OTHER INFORMATION: 3' nos
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (888)..(337)
; OTHER INFORMATION: coding region of the bar gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1721)..(889)
; OTHER INFORMATION: 35S promoter
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1991)..(1767)
; OTHER INFORMATION: 3' end 35S
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4511)..(2003)
; OTHER INFORMATION: coding region ispla
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4546)..(4515)
; OTHER INFORMATION: leader sequence from the corn GL4 transcript
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5732)..(4547)
; OTHER INFORMATION: corn preferential promoter GL4
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5989)..(5765)
; OTHER INFORMATION: 3' end 35S
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7228)..(6001)
; OTHER INFORMATION: isp2a coding region

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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (7263)..(7232)
;   OTHER INFORMATION: leader sequence of the GL4 transcript
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (8449)..(7264)
;   OTHER INFORMATION: corn root preferential promoter GL4
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (8514)..(8490)
;   OTHER INFORMATION: RB=right T-DNA border
US-10-623-500-12

Alignment Scores:
Pred. No.:                2.04e-05      Length:          8514
Score:                    129.50        Matches:         161
Percent Similarity:       31.87%        Conservative:    108
Best Local Similarity:    19.08%        Mismatches:      314
Query Match:              3.28%         Indels:          261
DB:                       6             Gaps:            42

US-09-494-297-2 (1-757) x US-10-623-500-12 (1-8514)

Qy         53 LeuValGluSerSerThrProAsnAlaIleAsnProAspSerSerSerGluTyr------ 70
              :::   :::      |||   |||   :::                    ||||||
Db       4382 ATCTACGACCAGCAGACCGCTAACACCCTCGTGGACCAGAAGCACCAGGAGTACCACTCC 4323

Qy         71 ---ArgTrpTyrGly---TyrGluSerTyrValArgGlyHisProTyrTyrLysGlnPhe 88
                ||||||   |||      :::|||         |||                  |||
Db       4322 ATCCGCTGGATCGGCCTGATCCAGTCCTCCGCCACTGGTGAC---------TTCACCTTC 4272

Qy         89 ArgValAlaHisAspLeuArgValAsnLeuGlu-------------------------- 99
              :::::::::   |||            :::|||
Db       4271 AAGCTGTCCGACGACGAGAACGCCATCATCGAGCTGGACGGCAAGGTGATCTCCGAGAAG 4212

Qy        100 GlySerArgSerTyrGlnValTyrCysPheAsnLeuLysLysAlaProLeuGlySer 119
              |||:::         |||:::        |||:::|||           |||
Db       4211 GGCAACAACAAGCAGTCCGTGCAC---------CTCGAAAAG-----------GGCCAG 4173

Qy        120 AspSerSerValLysLysTrpTyrLysLysHisAspGlyIleSerThrLysPheGluAsp 139
                  :::|||      |||:::      |||   :::            :::
Db       4172 CTGGTGCAGATCAAGATCGAGTACCAGTCCGACGACGCCCTGCACATCGACAACAAGATC 4113

Qy        140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159
              :::                        ||||||      ||||||      :::
Db       4112 TTC-----------------------AAGGAGCTG------AAGCTGTTCAAGATCGAC 4083

Qy        160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAla 179
                  |||   |||
Db       4082 TCCCAGAACCACTCCCAG---------------------------------------- 4065

Qy        180 IleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnPro 199
              :::|||   |||:::                          :::   ||||||
Db       4064 ---CAGGTGCAGCAGGAC-------------------------GAGCTGAGGAACCCA 4035

Qy        200 AspGluSerPheLysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeu 219
              |||      |||:::|||:::::      |||         |||:::   :::|||
Db       4034 ---GAGTTCAACAAGAAGGAGACCCAGGTGTTCCTGAAGAAGGCCTCCAAGACCAACCTG 3978

Qy        220 MetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGln 239
                    |||      |||:::   ||||||   :::      |||
Db       3977 TTCACCCAGAAGACCAAGAGGGACATCGACGAGGACACCGACACCGAC---GGCGACTCC 3921

Qy        240 ValProAspAspPheGlnLeuSerIlePheGluSerGluAspLys-------------- 254
              :::|||||||   ::::::   :::   :::      :::::::|||
Db       3920 ATCCCGGACGTGTGGGAGGAGAACGGCTACACCATCCAGAACAAGGTGGCCGTGAAGTGG 3861

Qy        255 ---GlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValProThr 273
                        :::|||||||||||||         |||         |||
Db       3860 GACGACTCCCTGGCCTCCAAGGGCTACCAGAAGTTCACCAGCAAC---------CCACTC 3810

Qy        274 LysProProThrProGlyAspProProMetProProAsnGlnProGlnThrThrSerVal 293
```

```
                 :::      |||   |||||||||
Db       3809 GAAGCCCACACCGTGGGCGACCCA---------------------------------- 3786

Qy        294 LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeuGluGlyAlaThrLeuGln 313
                                        ||||||   |||                  |||
Db       3785 ------------------TACTCCGACTACGAGAAGGCTGCTAGGGACATGCCACTGTCC 3744

Qy        314 LeuThrGlyAspAsnValAsn--------------------------------SerPhe 322
                     :::      |||                                  |||
Db       3743 AACGCCAAGGAGACCTTCAACCCACTGGTGGCTGCTTTCCCATCCGTGAACGTGTCCCTC 3684

Qy        323 GlnAlaArgValPheSerSerAsn---AspIleGlyGluArgIleGluLeuSerAspGly 341
                 :::      :::   |||   |||   |||:::        :::|||   |||
Db       3683 GAAAAGGTGATCCTGTCCAAGAACGAGGACCTGTCCCACTCCGTGGAGTCCTCCCAGTCC 3624

Qy        342 Thr---------TyrThrLeuThrGlu---LeuAsnSerProAlaGlyTyrSerIleAla 357
                |||         ||||||   ||||||   :::|||      ||||||:::|||
Db       3623 ACCAACTGGTCCTACACCAACACCGAGGGCGTGAACGTGAACGCTGGTTGGTCCGGTCTG 3564

Qy        358 GluPro---------------IleThrPheLys-------------------------- 363
                 |||               :::   ::::::
Db       3563 GGTCCATCCTTCGGCGTGTCCGTGAACTACCAGCACTCCGAGACCGTGGCCAACGAGTGG 3504

Qy        363 ------------------------------------------------------------ 363

Db       3503 GGCTCCGCCACCAACGACGGCACCCACATCAACGGTGCTGAGTCCGCCTACCTGAACGCC 3444

Qy        364 ------------------ValGluAlaGlyLysValTyrThr------------------ 371
                               |||      |||   :::|||
Db       3443 AACGTGAGGTACAACAACGTGGGCACCGGTGCTATCTACGAGACCAAGCCAACCACCTCC 3384

Qy        372 ---IleIleAspGlyLysGlnIle------------------GluAsnProAsnLysGlu 384
                 |||:::||||||      |||                  ||||||
Db       3383 TTCATCCTGGACGGCACCACCATCGGCACCATCAAGGCCAAGGAGAACACCACCGCTCTG 3324

Qy        385 IleValGluPro---------TyrSerValGlu---------------AlaTyrAsnAsp 396
                 :::   |||         |||      :::            |||   |||
Db       3323 ACCATCCTGCCAGACCAGTCCTACCCAGAGAAGGGCAAGAACGGCATCGCCATCAACACG 3264

Qy        397 PheGluGluPheSer------------------------------------------------ 401
                 ::::::|||:::
Db       3263 ATGGACGACTTCAACTCCAGGCCGATCCCACTGAACAAGGAGCAGCTGAACACCTACCTG 3204

Qy        402 ------------------ValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLys 415
                               :::|||   |||                  |||      |||
Db       3203 TCCAACAAGAAGCCGATCCTGCTCGAAACCGACCAGGTGGAGGGCAAGTACGCCATCAAG 3144

Qy        416 AsnLysAsnGlySerSerGlnValValTyrCysPheAsnAla---------------Asp 430
                 :::   ||||||:::      :::         :::|||
Db       3143 GACACCAACGGCAACATCACCATCGCTGGTGACTGGAACGGCATCACCGACGAGATCTCC 3084

Qy        431 LeuLysSerProProAspSerGluAspGlyGlyLysThrMetThr--------------- 445
                 |||:::                |||   |||      |||:::
Db       3083 GCCAAGACCGCCAGCATCATCGTCGACAACGGCAACCAGATGTCCGAGAAGAGGGTGGCT 3024

Qy        446 ---ProAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPhe 464
                    |||:::|||      |||   |||      :::::::::   ::::::
Db       3023 GCTAAGGACTACACCAACCCAGAGGACAAGACCCCAAATTTATCCGTGAAGGAGGCCCTG 2964

Qy        465 LysTyrThrValLysProArgAspThrAspProAspThrPheLeu--------------- 479
                 |||                           :::   |||      |||
Db       2963 AAGCTGGCCTACCCAGACGAGATCGAGGAGAAGGACGGCCTGCTGTTCTACAACGACCAG 2904

Qy        480 ---------------------------------LysHisIleLysLysValIleGlu 487
                                              ::::::      |||   |||
Db       2903 CCGATCTTCGAGGCTTCCGTGCAGTCCTACGTGGACGAGTACACCGCTAAGCAGATCAGG 2844

Qy        488 LysGlyTyrArgGluLys---GlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGln 506
                 |||         :::      |||         :::         |||   :::   :::
Db       2843 AAGCAGCTGAACGACTCCACCGGTTCCTTCAAGGACGTGAAGAACCTGTACGACGTGAAG 2784

Qy        507 LeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPheThr------AspSerAlaGluLeu 524
                 |||                  |||         |||      |||      |||
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```
Db       2783 CTCGAACCGAAGATGAACTTCACAATAAAGACCTCCACCCTGTACGACGGTGGTGAGTCC 2724

Qy        525 AspLysAspLysLeuLysAspTyrHis--------------------GlyPheGlyAsp 537
              |||      |||:::   :::::::::                    |||
Db       2723 GACAACACCAAGATCGGCAACTGGTACTACACCTACGTGGTGAACGGTGGTAACACCGGT 2664

Qy        538 MetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsn 557
                          |||                  |||   :::   :::|||
Db       2663 AAGAAGCAGTACAGGTCCGCTAACAAGGGTGCTTTCACCGAGCTGTCCACCGAGTCCAAG 2604

Qy        558 ProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeu 577
                        :::::::|||:::::::::            |||      |||
Db       2603 AACAAGCTGAAGAAGAACATCGACTACTACGTGTCCCTGTACATGAAGGCTGACTCCAAG 2544

Qy        578 IleGlyThrGlnTrpHisProGluAspLeuValAspIleIleArgMetGluAspLysLys 597
              :::                   .  ||||||   |||   ::::::   |||:::
Db       2543 GTGTCC----------------------GTGGAC---ATCGAGATCGACGGTAAGCAG 2511

Qy        598 GluValIleProValThrHisAsnLeuThrLeuArgLysThr------------------ 611
              |||   |||   ||||||   |||:::||||||
Db       2510 GAGTCCATC---GTGACCGACAACATCACCCTGGACCACGTGGGTTACCAGAGGATCAAC 2454

Qy        612 ------ValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeu 629
                    |||      |||   |||:::                          |||   :::
Db       2453 ATCCTGGTGCCAAACCTGGAGGGCAACGAGATCAAC------------ACCATCTCCATC 2406

Qy        630 LysAsnAsnLysGlnGluLeuLeu------------SerGlnThrValLysThrAspLys 645
              |||   :::   |||      :::                  |||:::
Db       2405 AAGGGTGACGGCCAGACCAACGTGTACTGGGACGACGTGTCCTTCGTGGAGGTGGGTGCT 2346

Qy        646 ThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGluSerLeu 665
                    :::|||:::||||||              ::::::      |||:::
Db       2345 GAGGAGATCGAGTACAAGGACCCAGTGCCACAGTTCGACATCATCGAGGGTGAC---TTC 2289

Qy        666 ThrLeuGlnGlyLeuProGluGlyTyrSerTyr--------------------------- 676
                  |||   |||           |||
Db       2288 GACTTCTTCGGTGACCCACTGGCCGTGAAGTACCACGACGCTACCTACTTCATCGACTCC 2229

Qy        677 ---LeuValLysGluThrAspSerGlu---GlyTyrLysValLysValAsnSerGlnGlu 694
                 |||:::   :::|||              :::      ||||||      ::::::
Db       2228 CCACTGATTACCCAGACCCCAGGTACCTTCTCCTTCACCTACAAGGTGATCGGTGAGCAG 2169

Qy        695 ValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGlu---ThrLeuAlaPhe 713
                          |||   :::|||      ::::::         |||   |||
Db       2168 ACCAAGACCGTGCTGGACTCCGGTTCCGGCAAGAACGCTAACAGGATCAACCTGGACTTC 2109

Qy        714 GluAsnAsnLys 717
              :::|||   |||
Db       2108 AAGAACGTGAAG 2097
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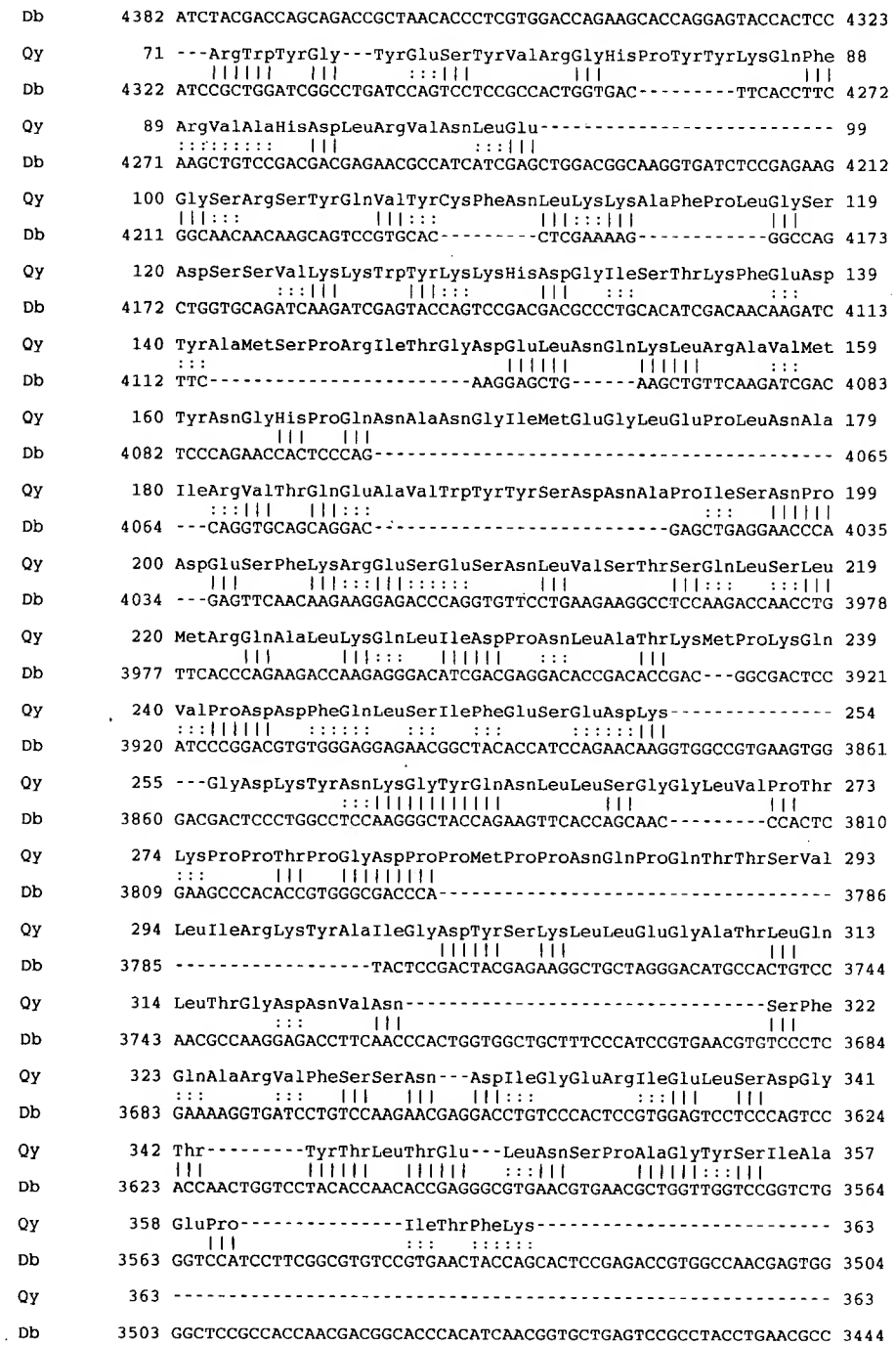
RESULT 11
US-10-623-500-13/c
; Sequence 13, Application US/10623500
; GENERAL INFORMATION:
; APPLICANT: Bayer BioScience N.V.
; APPLICANT: Greet, Vanderkimpen
; APPLICANT: Gerben, Van Eldik
; APPLICANT: Frank, Meulewaeter
; TITLE OF INVENTION: Corn root preferential promoters and uses thereof
; FILE REFERENCE: 021565-119
; CURRENT APPLICATION NUMBER: US/10/623,500
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 60/399383
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 8692
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pTW018 T-DNA sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (25)..(1)
; OTHER INFORMATION: LB= left border region (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (318)..(58)
; OTHER INFORMATION: 3' nos (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (888)..(337)
; OTHER INFORMATION: coding region of the bar gene (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1721)..(889)
; OTHER INFORMATION: 35S promoter (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1991)..(1767)
; OTHER INFORMATION: 3' 35S (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4511)..(2003)
; OTHER INFORMATION: coding region ispla (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4542)..(4518)
; OTHER INFORMATION: leader sequence from the corn GL5 transcript (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5822)..(4543)
; OTHER INFORMATION: GL5 promoter (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6078)..(5854)
; OTHER INFORMATION: 3' 35S (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7317)..(6090)
; OTHER INFORMATION: isp2a coding region (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7348)..(7324)
; OTHER INFORMATION: leader sequence of the corn GL5 transcript (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8628)..(7349)
; OTHER INFORMATION: promoter of the corn GL5 transcript (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8692)..(8668)
; OTHER INFORMATION: Right T-DNA border (complement)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5630)..(5630)
; OTHER INFORMATION: n=any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8436)..(8436)
; OTHER INFORMATION: n=any nucleotide
US-10-623-500-13

Alignment Scores:

Pred. No.:	2.12e-05	Length:	8692
Score:	129.50	Matches:	161
Percent Similarity:	31.87%	Conservative:	108
Best Local Similarity:	19.08%	Mismatches:	314
Query Match:	3.28%	Indels:	261
DB:	6	Gaps:	42

US-09-494-297-2 (1-757) x US-10-623-500-13 (1-8692)

```
Qy         53 LeuValGluSerSerThrProAsnAlaIleAsnProAspSerSerSerGluTyr------ 70
              :::   :::      |||   |||   :::                    ||||||
```


Db 4382 ATCTACGACCAGCAGACCGCTAACACCCTCGTGGACCAGAAGCACCAGGAGTACCACTCC 4323
Qy 71 ---ArgTrpTyrGly---TyrGluSerTyrValArgGlyHisProTyrTyrLysGlnPhe 88
Db 4322 ATCCGCTGGATCGGCCTGATCCAGTCCTCCGCCACTGGTGAC---------TTCACCTTC 4272
Qy 89 ArgValAlaHisAspLeuArgValAsnLeuGlu---------- 99
Db 4271 AAGCTGTCCGACGACGAGAACGCCATCATCGAGCTGGACGGCAAGGTGATCTCCGAGAAG 4212
Qy 100 GlySerArgSerTyrGlnValTyrCysPheAsnLeuLysLysAlaProLeuGlySer 119
Db 4211 GGCAACAACAAGCAGTCCGTGCAC---------CTCGAAAAG-----------GGCCAG 4173
Qy 120 AspSerSerValLysLysTrpTyrLysLysHisAspGlyIleSerThrLysPheGluAsp 139
Db 4172 CTGGTGCAGATCAAGATCGAGTACCAGTCCGACGACGCCCTGCACATCGACAACAAGATC 4113
Qy 140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159
Db 4112 TTC----------AAGGAGCTG------AAGCTGTTCAAGATCGAC 4083
Qy 160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAla 179
Db 4082 TCCCAGAACCACTCCCAG---------- 4065
Qy 180 IleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnPro 199
Db 4064 ---CAGGTGCAGCAGGAC----------GAGCTGAGGAACCCA 4035
Qy 200 AspGluSerPheLysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeu 219
Db 4034 ---GAGTTCAACAAGAAGGAGACCCAGGTGTTCCTGAAGAAGGCCTCCAAGACCAACCTG 3978
Qy 220 MetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGln 239
Db 3977 TTCACCCAGAAGACCAAGAGGGACATCGACGAGGACACCGACACCGAC---GGCGACTCC 3921
Qy 240 ValProAspAspPheGlnLeuSerIlePheGluSerGluAspLys---------- 254
Db 3920 ATCCCGGACGTGTGGGAGGAGAACGGCTACACCATCCAGAACAAGGTGGCCGTGAAGTGG 3861
Qy 255 ---GlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValProThr 273
Db 3860 GACGACTCCCTGGCCTCCAAGGGCTACCAGAAGTTCACCAGCAAC---------CCACTC 3810
Qy 274 LysProProThrProGlyAspProProMetProProAsnGlnProGlnThrThrSerVal 293
Db 3809 GAAGCCCACACCGTGGGCGACCCA---------- 3786
Qy 294 LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeuGluGlyAlaThrLeuGln 313
Db 3785 ----------TACTCCGACTACGAGAAGGCTGCTAGGGACATGCCACTGTCC 3744
Qy 314 LeuThrGlyAspAsnValAsn----------SerPhe 322
Db 3743 AACGCCAAGGAGACCTTCAACCCACTGGTGGCTGCTTTCCCATCCGTGAACGTGTCCCTC 3684
Qy 323 GlnAlaArgValPheSerSerAsn---AspIleGlyGluArgIleGluLeuSerAspGly 341
Db 3683 GAAAAGGTGATCCTGTCCAAGAACGAGGACCTGTCCCACTCCGTGGAGTCCTCCCAGTCC 3624
Qy 342 Thr---------TyrThrLeuThrGlu---LeuAsnSerProAlaGlyTyrSerIleAla 357
Db 3623 ACCAACTGGTCCTACACCAACACCGAGGGCGTGAACGTGAACGCTGGTTGGTCCGGTCTG 3564
Qy 358 GluPro----------IleThrPheLys---------- 363
Db 3563 GGTCCATCCTTCGGCGTGTCCGTGAACTACCAGCACTCCGAGACCGTGGCCAACGAGTGG 3504
Qy 363 ---------- 363
Db 3503 GGCTCCGCCACCAACGACGGCACCCACATCAACGGTGCTGAGTCCGCCTACCTGAACGCC 3444
Qy 364 ----------ValGluAlaGlyLysValTyrThr---------- 371
Db 3443 AACGTGAGGTACAACAACGTGGGCACCGGTGCTATCTACGAGACCAAGCCAACCACCTCC 3384
Qy 372 ---IleIleAspGlyLysGlnIle----------GluAsnProAsnLysGlu 384
Db 3383 TTCATCCTGGACGGCACCACCATCGGCACCATCAAGGCCAAGGAGAACACCACCGCTCTG 3324
Qy 385 IleValGluPro---------TyrSerValGlu----------AlaTyrAsnAsp 396
Db 3323 ACCATCCTGCCAGACCAGTCCTACCCAGAGAAGGGCAAGAACGGCATCGCCATCAACACG 3264
Qy 397 PheGluGluPheSer---------- 401
Db 3263 ATGGACGACTTCAACTCCAGGCCGATCCCACTGAACAAGGAGCAGCTGAACACCTACCTG 3204
Qy 402 ----------ValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLys 415
Db 3203 TCCAACAAGAAGCCGATCCTGCTCGAAACCGACCAGGTGGAGGGCAAGTACGCCATCAAG 3144
Qy 416 AsnLysAsnGlySerSerGlnValValTyrCysPheAsnAla----------Asp 430
Db 3143 GACACCAACGGCAACATCACCATCGCTGGTGACTGGAACGGCATCACCGACGAGATCTCC 3084
Qy 431 LeuLysSerProProAspSerGluAspGlyGlyLysThrMetThr---------- 445
Db 3083 GCCAAGACCGCCAGCATCATCGTCGACAACGGCAACCAGATGTCCGAGAAGAGGGTGGCT 3024
Qy 446 ---ProAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPhe 464
Db 3023 GCTAAGGACTACACCAACCCAGAGGACAAGACCCCAAATTTATCCGTGAAGGAGGCCCTG 2964
Qy 465 LysTyrThrValLysProArgAspThrAspProAspThrPheLeu---------- 479
Db 2963 AAGCTGGCCTACCCAGACGAGATCGAGGAGAAGGACGGCCTGCTGTTCTACAACGACCAG 2904
Qy 480 ----------LysHisIleLysLysValIleGlu 487
Db 2903 CCGATCTTCGAGGCTTCCGTGCAGTCCTACGTGGACGAGTACACCGCTAAGCAGATCAGG 2844
Qy 488 LysGlyTyrArgGluLys---GlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGln 506
Db 2843 AAGCAGCTGAACGACTCCACCGGTTCCTTCAAGGACGTGAAGAACCTGTACGACGTGAAG 2784
Qy 507 LeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPheThr------AspSerAlaGluLeu 524
Db 2783 CTCGAACCGAAGATGAACTTCACAATAAAGACCTCCACCCTGTACGACGGTGGTGAGTCC 2724
Qy 525 AspLysAspLysLeuLysAspTyrHis----------GlyPheGlyAsp 537
Db 2723 GACAACACCAAGATCGGCAACTGGTACTACACCTACGTGGTGAACGGTGGTAACACCGGT 2664
Qy 538 MetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsn 557
Db 2663 AAGAAGCAGTACAGGTCCGCTAACAAGGGTGCTTTCACCGAGCTGTCCACCGAGTCCAAG 2604
Qy 558 ProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeu 577
Db 2603 AACAAGCTGAAGAAGAACATCGACTACTACGTGTCCCTGTACATGAAGGCTGACTCCAAG 2544
Qy 578 IleGlyThrGlnTrpHisProGluAspLeuValAspIleIleArgMetGluAspLysLys 597
Db 2543 GTGTCC----------GTGGAC---ATCGAGATCGACGGTAAGCAG 2511
Qy 598 GluValIleProValThrHisAsnLeuThrLeuArgLysThr---------- 611
Db 2510 GAGTCCATC---GTGACCGACAACATCACCCTGGACCACGTGGGTTACCAGAGGATCAAC 2454
Qy 612 ------ValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeu 629
Db 2453 ATCCTGGTGCCAAACCTGGAGGGCAACGAGATCAAC----------ACCATCTCCATC 2406

```
Qy        630 LysAsnAsnLysGlnGluLeuLeu-----------SerGlnThrValLysThrAspLys 645
Db       2405 AAGGGTGACGGCCAGACCAACGTGTACTGGGACGACGTGTCCTTCGTGGAGGTGGGTGCT 2346

Qy        646 ThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGluSerLeu 665
Db       2345 GAGGAGATCGAGTACAAGGACCCAGTGCCACAGTTCGACATCATCGAGGGTGAC---TTC 2289

Qy        666 ThrLeuGlnGlyLeuProGluGlyTyrSerTyr-------------------------- 676
Db       2288 GACTTCTTCGGTGACCCACTGGCCGTGAAGTACCACGACGCTACCTACTTCATCGACTCC 2229

Qy        677 ---LeuValLysGluThrAspSerGlu---GlyTyrLysValLysValAsnSerGlnGlu 694
Db       2228 CCACTGATTACCCAGACCCCAGGTACCTTCTCCTTCACCTACAAGGTGATCGGTGAGCAG 2169

Qy        695 ValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGlu---ThrLeuAlaPhe 713
Db       2168 ACCAAGACCGTGCTGGACTCCGGTTCCGGCAAGAACGCTAACAGGATCAACCTGGACTTC 2109

Qy        714 GluAsnAsnLys 717
Db       2108 AAGAACGTGAAG 2097

RESULT 12
US-10-450-826-4
; Sequence 4, Application US/10450826
; GENERAL INFORMATION:
;  APPLICANT: Ji, Darren
;  APPLICANT:  Axelrod, Douglas W.
;  APPLICANT:  Cook, Jonathon S.
;  APPLICANT:  Jaiswal, Neelam
;  APPLICANT:  Eistein, Richard
;  APPLICANT:  Houghton, Adam
;  APPLICANT:  Mertz, Lawrence
;  TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiati
;  FILE REFERENCE: 044921-5039-WO
;  CURRENT APPLICATION NUMBER: US/10/450,826
;  CURRENT FILING DATE:  2003-06-18
;  PRIOR APPLICATION NUMBER: US 60/255,882
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: US 60/285,691
;  PRIOR FILING DATE: 2001-04-24
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 4925
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. AF155135
US-10-450-826-4

Alignment Scores:
Pred. No.:              8.57e-06      Length:          4925
Score:                  129.00        Matches:         150
Percent Similarity:     36.79%        Conservative:    102
Best Local Similarity:  21.90%        Mismatches:      263
Query Match:            3.27%         Indels:          171
DB:                     6             Gaps:            36

US-09-494-297-2 (1-757) x US-10-450-826-4 (1-4925)

Qy        124 LysLysTrpTyrLysLysHis---AspGlyIleSerThrLysPheGluAspTyr------ 140
Db        906 AAGAAGTGGAACTCCAAAAACACGCAAAGCTCCACCACCTCCTATCAGTCCTACCCAGTT 965

Qy        141 ------AlaMet-SerProArg---IleThrGlyAspGluLeuAsnGlnLysLeuArgAl 157
Db        966 GAGTGATGTCTCTTCCCCAAGATCAATAACTTCGACTCCACTATCGGGAAAG---GAATC 1022

Qy        157 aValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLe 177

Db       1023 GGTATTTTTTGCTGAACCACCCTTCAAGGCTGAG-----------------------AT 1058

Qy        177 uAsnAlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSe 197
Db       1059 CAGTTCTATACGAGAAAACAAAGACAGACTA---------AGTGACAGTACT------AC 1103

Qy        197 rAsnProAspGluSerPheLysArgGluSerGluSer---------AsnLeuValSerTh 214
Db       1104 AGGTGCTGATAGCTTATTGGATATAAGTTCTGAAGCTGACCAACAAGATCTTCTCTCTCT 1163

Qy        214 rSerGlnLeuSerLeuMetArgGlnAlaLeu------LysGlnLeuIleAspProAsnLe 232
Db       1164 ATTGCAAGCAAAAGTTGCTTCCCTTACCTTACACAATAAGGAGTTACAAGAT---AAATT 1220

Qy        232 uAlaThrLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSer-- 251
Db       1221 ACAGGCCAAATCACCCAAGGAGGCGGAAGCAGACCTAAGCTTTGACTCATACCATTCCAC 1280

Qy        252 ----GluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLe 270
Db       1281 CCAAACTGACTTGGGCCCATCCCTGGGAAAA---------------------------- 1311

Qy        270 uValProThrLysProProThrProGlyAspProProMetProProAsnGlnProGlnTh 290
Db       1312 ----------------------CCTGGTGAA---ACCTCTCCCCCAGACTCCAAATCATC 1346

Qy        290 rThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeuGluGlyAl 310
Db       1347 TCCATCTGTCTTAATA------CATTCTTTAGGTAAA---TCCACTACTGACAATGATGT 1397

Qy        310 aThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAs 330
Db       1398 CAGAATTCAGCAACTGCAAGAGATTTTGCAAGATCTACAGAAGAGATTAGAGAGCTCTGA 1457

Qy        330 nAspIleGlyGluArg-----------IleGluLeuSerAspGlyThrTyrThrLeuTh 346
Db       1458 A------GCAGAGAGAAAACAGCTACAGGTCGAACTCCAATCCCGAAGGGCAGAACTGGT 1511

Qy        346 rGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAl 366
Db       1512 ATGCTTAAACAACACTGAGATTTCAGAGAACAGCTCTGACCTCAGCCAGAAACTTAAAGA 1571

Qy        366 aGlyLysValTyrThrIleIleAspGlyLysGlnIleGluAsnProAsnLysGlu----- 384
Db       1572 AACTCAGAGCAAATACGAGGAGGCTATGAAAGAAGTCCTTAGTGTGCAGAAGCAGATGAA 1631

Qy        385 -------IleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPheServa 402
Db       1632 ACTCGGTCTTGTCTCACCTGAAAGCATGGATAATTATTCACATTTCCACGAGCTGAGGGT 1691

Qy        402 lLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGl 422
Db       1692 CACGGAAGAGGA-AATAAATGTGCT-----------------AAAGCAGGATCTGCAGA 1732

Qy        422 nValValTyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAsp---GlyGl 441
Db       1733 A---------TGCATTAGAAGAAAGTGAAAGAAATAAAGAGAAAGTGAGAGAGTTAGAGG 1783

Qy        441 yLysThrMetThrProAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyAr 461
Db       1784 AAAAACT-------------------------------------------------GGTAG 1795

Qy        461 gAspLeuPheLysTyrThr-ValLysProArgAspThrAspProAspThrPheLeuLysH 481
Db       1796 AGAGGGAGAAAGGTACAGTGATTAAGCCACCTGTGGAAGAGTACGAGGAAATGAAAAGTT 1855

Qy        481 isIleLysLysValIleGluLysGlyTyrArgGluLysGlyGlnAlaIle---------- 497
Db       1856 CATATTGCTCTGTTATTGAGAATATGAATAAGGAGAAAGCATTTTTGTTTGAGAAATACC 1915

Qy        498 -------------GluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnL 513
Db       1916 AAGAAGCCCAAGAAGAAATCATGAAATTAAAAGACACACTAAAAAGTCAGATGACACAGG 1975
```

```
Qy         513 euAlaIleTyrTyrPheThrAspSerAla------------------------------ 522
                  |||             ::|||   |||
Db        1976 AAGCC------------AGTGATGAAGCTGAGGACATGAAAGAAGCCATGAATAGGATGA 2023

Qy         523 -----GluLeuAspLysAsp-------------------------------------L 528
                    |||||:::|||                                         :
Db        2024 TAGATGAACTCAATAAACAGGTGAGCGAGCTGTCACAGCTGTACAAAGAAGCCCAGGCTG 2083

Qy         528 ysLeuLysAspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysI 548
               ::|||:::||||||                ::::    |||    |||
Db        2084 AGCTGGAGGATTACAGGAAGAGGAAATCTCTAGAGGATGTCACA--------------- 2127

Qy         548 leLeuValGluTyr---------AlaGlnAspSerAsnProProGlnLeuThrAspLeu- 564
                        ||||||          |||:::                ||||||||||:::::
Db        2128 -----GCTGAATATATCCATAAAGCAGAGCATGAGAAACTGATGCAATTGACAAACGTGT 2182

Qy         565 -----------------AspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIleG 579
                                |||               ::::::|||      ::::::
Db        2183 CCAGGGCTAAAGCAGAAGATGCACTGTCTGAAATGAAGTCTCAGTATTCAAAAGTGTTGA 2242

Qy         579 lyThrGlnTrpHisProGluAspLeuValAspIleIleArgMetGluAspLysLysGluV 599
                                :::   |||||||||                |||:::
Db        2243 ATGAGTTGACCCAGCTCAAACAACTGGTGGAT------------GCACAAAAAGAGAACT 2290

Qy         599 alIleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspA 619
                 :::    :::|||  :::|||   :::        |||:::                |
Db        2291 CTGTCTCTATCACAGAACATTTGCAAGTGATAACCACGCTG------------------C 2332

Qy         619 rgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerG 639
               |||||                  |||    ::::::  |||    |||:::  |||    |||:
Db        2333 GGACTGCAGCAAAAGAGATGGAAGAAAAAAATAAGCAATCTTAAGGAACACCTTGCAAGCA 2392

Qy         639 lnThrValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnL 659
               ::    |||:::        |||        :::      :::    ||||||
Db        2393 AGGAAGTGGAAGTAGCAAAGCTGGAGAAACAACTCTTAGAAGAGAAAGCT---------- 2442

Qy         659 euLysHisGlyGluSerLeuThrLeuGlnGlyLeuPro---GluGlyTyrSerTyrLeuV 678
                                  ::::::|||        :::|||          |||      |||
Db        2443 --------------GCTATGACTGATGCAATGGTACCTCGGTCTTCCTATGAAAAACTCC 2488

Qy         678 alLysGluThrAspSerGluGlyTyrLysValLysValAsnSerGlnGluValAlaAsnA 698
                           :::||||||          |||     |||     :::     ::::::      :
Db        2489 AGTCATCCTTAGAGAGTGAA---------GTGAGTGTGTTGGCATCGAAATTAAAGGAAT 2539

Qy         698 laThrValSerLysThrGlyIleThrSerAsp-----------------GluThrLeuA 712
               ::          |||     :::     |||:::                     |||
Db        2540 CTGTGAAAGAGAAAGAGAAGGTCCATTCAGAGGTTGTCCAGATTAGAAGTGAGGTCTCAC 2599

Qy         712 laPheGluAsnAsnLysGluProVal------ValProThrGlyValAspGlnLysIleA 730
                    :::        ||||||      :::           :::              :::|||::::::|
Db        2600 AGGTGAAAAGAGAAAAGGAAATATTCAGACTCTCTTGAAATCCAAAGAGCAAGAAGTAA 2659

Qy         730 snGlyTyrLeu 733
               ||       |||
Db        2660 ATGAACTTCTG 2670
```

RESULT 13
US-10-105-837-480
; Sequence 480, Application US/10105837
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qing A.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BDIVA
; CURRENT APPLICATION NUMBER: US/10/105,837
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 480
; LENGTH: 4226
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2982)
US-10-105-837-480

```
Alignment Scores:
Pred. No.:                8.85e-06       Length:         4226
Score:                    128.00         Matches:        145
Percent Similarity:       32.41%         Conservative:   89
Best Local Similarity:    20.08%         Mismatches:     232
Query Match:              3.24%          Indels:         256
DB:                       6              Gaps:           35
```

US-09-494-297-2 (1-757) x US-10-105-837-480 (1-4226)

```
Qy          85 TyrLysGlnPheArgValAlaHisAspLeuArg------ValAsnLeuGlu---GlySer 101
               :::|||   ||||||:::    |||    |||                |||:::|||   |||:::
Db          64 TTTAAGTTATTCAGACTTGTACACAAACTTGGAGGATTTGATAATATTGAAAGTGGAGCT 123

Qy         102 ArgSerTyrGlnValTyrCysPheAsnLeuLysLysAlaPheProLeu---------Gly 118
                           |||||||||                |||:::
Db         124 GTTTGGAAACAAGTCTAC---------CAAGATCTTGGAATCCCTGTCTTAAATTCAGCT 174

Qy         119 SerAspSerSerValLysLysTrpTyrLysLysHisAspGlyIleSerThrLysPheGlu 138
               :::      :::||||||     |||||||||:::                      ||||||
Db         175 GCAGGATACAATGTTAAATGTGCTTATAAAAAATAC---------TTATATGGTTTGAG 225

Qy         139 AspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaVal 158
               :::|||     ||||||   |||              |||             |||
Db         226 GAGTACTGTAGATCACCCAACATT---------GAATTTCAGATGGCATTGCCAGAGAAA 276

Qy         159 MetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsn 178
               :::   |||        :::              :::   |||
Db         277 GTTGTTAACAAGCAATGTAAGGAGTGTGAAAATGTAAAAGAA------------------ 318

Qy         179 AlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsn 198
                  |||:::|||   :::|||                                    |||
Db         319 ---ATAAAAGTTAAGGAGGAA----------------------------------AAT 339

Qy         199 ProAspGlu------SerPheLysArgGluSerGluSerAsnLeuValSerThrSerGln 216
                     |||            |||   |||   |||   |||::::::          :::
Db         340 GAAACAGAGATCCAAGAAATAAAGATGGAGGAGGAGAGGAATATAATACCAAGAGAAGAA 399

Qy         217 LeuSerLeuMetArgGln---AlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLys 235
                     :::      :::            |||:::   |||   |||:::|||   :::|||
Db         400 AAGCCTATTGAGGATGAAATTGAAAGAAAAGAAAATATTAAGCCCTCTCTGGGAAGTAAA 459

Qy         236 MetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSerGluAspLysGly 255

Db         459 ------------------------------------------------------------ 459

Qy         256 AspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValProThrLysPro 275
                                    :::|||||||||
Db         460 --------------------AAGAATTTATTAGAATCT-------------------- 477

Qy         276 ProThrProGlyAspProProMetProProAsnGlnProGlnThrThrSerValLeuIle 295
                                   :::|||   :::         |||          |||   |||
Db         478 --------------------ATACCTACACATTCTGATCAGGAAAAAGAAGTTAACATT 516

Qy         296 ArgLysTyrAlaIleGlyAspTyrSerLysLeuLeuGluGlyAlaThrLeuGlnLeuThr 315
               :::|||
Db         517 AAAAAA---------------------------------------------------CCA 525
```

```
Qy       316 GlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIleGlyGluArg 335
Db       526 GAAGACAATGAAAAT---------------------------------------------- 540

Qy       336 IleGluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSer 355
Db       541 ------CTGGATGACAAAGATGATGACACAACTAGGGTAGAT------------------- 576

Qy       356 IleAlaGluProIleThrPheLysValGluAlaGlyLysValTyrThrIleIleAspGly 375
Db       577 ------GAATCCCTCAACATAAAGGTAGAAGCTGAGGAAGAA------------AAAGCA 618

Qy       376 LysGlnIleGluAsnProAsnLys----------------------------------- 383
Db       619 AAATCTGGAGATGAAACGAATAAAGAAGAAGATGAAGATGATGAAGAAGCAGAAGAGGAG 678

Qy       384 ------------GluIleValGluProTyrSerValGluAlaTyrAsnAspPheGluGlu 399
Db       679 GAGGAGGAGGAAGAAGAAGAAGAGGATGAAGATGATGATGACAACAATGAGGAAGAGGAG 738

Qy       400 PheSerValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGly 419
Db       739 TTTGAGTGCTATCCACCAGGCATGAAAGTCCAAGTGCGGTATGGACGAGGGAAAAAT--- 795

Qy       420 SerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAsp 439
Db       796 ------CAAAAAATGTAT------GAAGCTAGTATTAAA---------GATTCTGATGTC 834

Qy       440 GlyGlyLysThrMetThrProAspPheThrThrGlyGluValLysTyr---ThrHisIle 458
Db       835 GAAGGT--------------------------GGAGAGGTCCTTTACTTGGTGCATTAC 867

Qy       459 AlaGlyArgAspLeuPheLysTyr----------------------ThrValLysPro 470
Db       868 TGCGGATGGAATGTG---AGATACGATGAATGGATTAAAGCAGATAAAATAGTAAGACCT 924

Qy       471 ArgAspThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLysGlyTyr 490
Db       925 GCTGATAAAAATGTGCCAAAG---ATAAAACATCGGAAGAAAATAAAGAATAAATTAGAC 981

Qy       491 ArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAla 510
Db       982 AAAGAAAAAGACAAAGATGAAAAATACTCTCCA---AAAAACTGTAAACTTCGG------ 1032

Qy       511 ThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLys 530
Db      1033 ----------------------------------CGCTTGTCCAAACCACCATTTCAG 1056

Qy       531 AspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuVal 550
Db      1057 --------------------ACAAATCCATCTCCTGAAATGGTATCCAAACTGGATCTC 1095

Qy       551 GluTyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsn 570
Db      1096 ACTGATGCCAAAAACTCTGATACTGCTCATATTAAGTCCATAGAAATT------------ 1143

Qy       571 AsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAspLeuValAspIle 590
Db      1144 ------------ACTTCGATCCTTAATGGACTTCAAGCTTCTGAAAGTTCTGCTGAAGAC 1191

Qy       591 IleArgMetGluAspLysLysGluValIleProValThrHisAsnLeuThrLeuArgLys 610
Db      1192 AGTGAGCAGGAAGATGAGAGAGGTGCTCAAGACATGGATAATAAT--------------- 1236

Qy       611 ThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeuLys 630
Db      1237 --------------GGCAAAGAGGAATCTAAGATTGATCAT------------TTGACC 1269

Qy       631 AsnAsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPhe 650
Db      1270 AACAACAGAAATGATCTTATTTCAAAGGAGGAACAGAACAGTTCATCTTTGCTAGAAGAA 1329

Qy       651 LysAspGlyLysAlaThrIleAsnLeuLysHisGlyGluSerLeuThrLeuGlnGlyLeu 670

Db      1330 AACAAAGTTCATGCAGATTTGGTAATATCCAAACCAGTGTCAAAATCTCCAGAAAGATTA 1389

Qy       671 ProGluGlyTyrSerTyrLeuValLysGluThrAspSerGluGlyTyrLysValLysVal 690
Db      1390 AGGAAAGATATAGAAGTATTATCCGAAGATACTGATTATGAAGAAGATGAAGTCACAAAA 1449

Qy       691 AsnSerGlnGluValAlaAsnAlaThrValSer--------------------------- 701
Db      1450 AAGAGAAAGGATGTCAAGAAGGACACAACAGATAAATCTTCAAAACCACAAATAAAACGT 1509

Qy       702 -----------------------------------LysThrGly-------------- 704
Db      1510 GGTAAAAGAAGGTATTGCAATACAGAAGAGTGTCTAAAAACTGGATCACCTGGCAAAAAG 1569

Qy       705 ---------IleThrSerAspGluThrLeuAlaPheGluAsnAsn-------------- 716
Db      1570 GAAGAGAAGGCCAAGAACAAAGAATCACTTTGCATGGAAAACAGTAGCAACAGCTCTTCA 1629

Qy       717 --------------------LysGluProValValProThrGlyValAspGlnLysIle 729
Db      1630 GATGAAGATGAAGAAGAAACAAAAGCAAAGATGACACCAACT---------AAGAAATAC 1680

Qy       730 AsnGly 731
Db      1681 AATGGT 1686
```

RESULT 14
US-10-286-897-796
; Sequence 796, Application US/10286897
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/286,897
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 796
; LENGTH: 4226
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2982)
US-10-286-897-796

Alignment Scores:

Pred. No.:	8.85e-06	Length:	4226
Score:	128.00	Matches:	145
Percent Similarity:	32.41%	Conservative:	89
Best Local Similarity:	20.08%	Mismatches:	232
Query Match:	3.24%	Indels:	256
DB:	6	Gaps:	35

US-09-494-297-2 (1-757) x US-10-286-897-796 (1-4226)

```
Db       1681 AATGGT 1686

RESULT 15
US-10-258-898A-796
; Sequence 796, Application US/10258898A
; GENERAL INFORMATION:
;  APPLICANT: Hyseq Inc
;  TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
;  FILE REFERENCE: 784FLPCT
;  CURRENT APPLICATION NUMBER: US/10/258,898A
;  CURRENT FILING DATE:  2002-10-29
;  PRIOR APPLICATION NUMBER: US/09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US09/598,042
;  PRIOR FILING DATE: 2000-06-20
;  PRIOR APPLICATION NUMBER: US09/620,312
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: US09/653,450
;  PRIOR FILING DATE: 2000-08-31
;  PRIOR APPLICATION NUMBER: US09/662,191
;  PRIOR FILING DATE: 2000-09-14
;  PRIOR APPLICATION NUMBER: US09/693,036
;  PRIOR FILING DATE: 2000-10-19
;  PRIOR APPLICATION NUMBER: US09/727,344
;  PRIOR FILING DATE: 2000-11-29
;  NUMBER OF SEQ ID NOS: 7143
;  SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 796
;   LENGTH: 4226
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2982)
US-10-258-898A-796

Alignment Scores:
Pred. No.:              8.85e-06        Length:         4226
Score:                  128.00          Matches:        145
Percent Similarity:     32.41%          Conservative:   89
Best Local Similarity:  20.08%          Mismatches:     232
Query Match:            3.24%           Indels:         256
DB:                     6               Gaps:           35

US-09-494-297-2 (1-757) x US-10-258-898A-796 (1-4226)

Qy         85 TyrLysGlnPheArgValAlaHisAspLeuArg------ValAsnLeuGlu---GlySer 101
              :::|||   ||||||:::   |||   |||           |||:::|||   |||:::
Db         64 TTTAAGTTATTCAGACTTGTACACAAACTTGGAGGATTTGATAATATTGAAAGTGGAGCT 123

Qy        102 ArgSerTyrGlnValTyrCysPheAsnLeuLysLysAlaProLeu---------Gly 118
                  |||||||||                 |||:::
Db        124 GTTTGGAAACAAGTCTAC---------CAAGATCTTGGAATCCCTGTCTTAAATTCAGCT 174

Qy        119 SerAspSerSerValLysLysTrpTyrLysLysHisAspGlyIleSerThrLysPheGlu 138
              :::      :::||||||     ||||||||||:::                ||||||
Db        175 GCAGGATACAATGTTAAATGTGCTTATAAAAAATAC---------TTATATGGTTTTGAG 225

Qy        139 AspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaVal 158
              :::|||      ||||||   |||         |||           |||
Db        226 GAGTACTGTAGATCACCCAACATT---------GAATTTCAGATGGCATTGCCAGAGAAA 276

Qy        159 MetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsn 178
              :::   |||      :::         :::   |||
Db        277 GTTGTTAACAAGCAATGTAAGGAGTGTGAAAATGTAAAAGAA----------------- 318

Qy        179 AlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsn 198
                 |||:::|||   :::|||                                   |||
Db        319 ---ATAAAAGTTAAGGAGGAA---------------------------------AAT 339

Qy        199 ProAspGlu------SerPheLysArgGluSerGluSerAsnLeuValSerThrSerGln 216
                           |||   |||   |||   |||::::::         :::
Db        340 GAAACAGAGATCCAAGAAATAAAGATGGAGGAGGAGAGGAATATAATACCAAGAGAAGAA 399

Qy        217 LeuSerLeuMetArgGln---AlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLys 235
              :::      :::         |||:::   |||   |||:::|||   :::|||
Db        400 AAGCCTATTGAGGATGAAATTGAAAGAAAAGAAAATATTAAGCCCTCTCTGGGAAGTAAA 459

Qy        236 MetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSerGluAspLysGly 255

Db        459 ------------------------------------------------------------ 459

Qy        256 AspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValProThrLysPro 275
                              :::||||||||||
Db        460 ---------------------AAGAATTTATTAGAATCT--------------------- 477

Qy        276 ProThrProGlyAspProProMetProProAsnGlnProGlnThrThrSerValLeuIle 295
                              :::|||   :::      |||         |||   |||
Db        478 ---------------------ATACCTACACATTCTGATCAGGAAAAAGAAGTTAACATT 516

Qy        296 ArgLysTyrAlaIleGlyAspTyrSerLysLeuLeuGluGlyAlaThrLeuGlnLeuThr 315
              :::|||
Db        517 AAAAAA----------------------------------------------------CCA 525

Qy        316 GlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIleGlyGluArg 335
                ||||||   |||
Db        526 GAAGACAATGAAAAT---------------------------------------------- 540

Qy        336 IleGluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSer 355
                    |||   |||               |||   ::::::
Db        541 ------CTGGATGACAAAGATGATGACACAACTAGGGTAGAT----------------- 576

Qy        356 IleAlaGluProIleThrPheLysValGluAlaGlyLysValTyrThrIleIleAspGly 375
                    |||   :::      ||||||||||||   :::
Db        577 ------GAATCCCTCAACATAAAGGTAGAAGCTGAGGAAGAA-----------AAAGCA 618

Qy        376 LysGlnIleGluAsnProAsnLys---------------------------------- 383
                 |||      :::      ||||||
Db        619 AAATCTGGAGATGAAACGAATAAAGAAGAAGATGAAGATGATGAAGAAGCAGAAGAGGAG 678

Qy        384 ------------GluIleValGluProTyrSerValGluAlaTyrAsnAspPheGluGlu 399
                         |||      |||         :::      |||:::   ||||||
Db        679 GAGGAGGAGGAAGAAGAAGAAGAGGATGAAGATGATGATGACAACAATGAGGAAGAGGAG 738

Qy        400 PheSerValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGly 419
              |||                     :::      |||   :::   ||||||
Db        739 TTTGAGTGCTATCCACCAGGCATGAAAGTCCAAGTGCGGTATGGACGAGGGAAAAAT--- 795

Qy        420 SerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAsp 439
                 |||   :::|||         |||   :::|||         |||||:::
Db        796 ------CAAAAAATGTAT------GAAGCTAGTATTAAA---------GATTCTGATGTC 834

Qy        440 GlyGlyLysThrMetThrProAspPheThrThrGlyGluValLysTyr---ThrHisIle 458
                 |||                        |||||||||   |||      |||
Db        835 GAAGGT--------------------------GGAGAGGTCCTTTACTTGGTGCATTAC 867

Qy        459 AlaGlyArgAspLeuPheLysTyr----------------------ThrValLysPro 470
                 |||   ::::::   :::|||                     |||:::|||
Db        868 TGCGGATGGAATGTG---AGATACGATGAATGGATTAAAGCAGATAAAATAGTAAGACCT 924

Qy        471 ArgAspThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLysGlyTyr 490
                 |||   :::            :::|||||||   ||||||:::      |||
Db        925 GCTGATAAAAATGTGCCAAAG---ATAAAACATCGGAAGAAAATAAAGAATAAATTAGAC 981

Qy        491 ArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAla 510
              :::|||||   :::      :::||||||              :::||||||
Db        982 AAAGAAAAAGACAAAGATGAAAAATACTCTCCA---AAAAACTGTAAACTTCGG------ 1032

Qy        511 ThrGlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLys 530
                                                  |||   |||         :::
Db       1033 ----------------------------------CGCTTGTCCAAACCACCATTTCAG 1056

Qy        531 AspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuVal 550
                                  |||   |||         |||:::|||:::   :::
```

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Db       1057 ----------------------ACAAATCCATCTCCTGAAATGGTATCCAAACTGGATCTC 1095

Qy        551 GluTyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsn 570

Db       1096 ACTGATGCCAAAAACTCTGATACTGCTCATATTAAGTCCATAGAAATT------------ 1143

Qy        571 AsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAspLeuValAspIle 590

Db       1144 ------------ACTTCGATCCTTAATGGACTTCAAGCTTCTGAAAGTTCTGCTGAAGAC 1191

Qy        591 IleArgMetGluAspLysLysGluValIleProValThrHisAsnLeuThrLeuArgLys 610

Db       1192 AGTGAGCAGGAAGATGAGAGAGGTGCTCAAGACATGGATAATAAT-------------- 1236

Qy        611 ThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeuLys 630

Db       1237 --------------GGCAAAGAGGAATCTAAGATTGATCAT------------TTGACC 1269

Qy        631 AsnAsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPhe 650

Db       1270 AACAACAGAAATGATCTTATTTCAAAGGAGGAACAGAACAGTTCATCTTTGCTAGAAGAA 1329

Qy        651 LysAspGlyLysAlaThrIleAsnLeuLysHisGlyGluSerLeuThrLeuGlnGlyLeu 670

Db       1330 AACAAAGTTCATGCAGATTTGGTAATATCCAAACCAGTGTCAAAATCTCCAGAAAGATTA 1389

Qy        671 ProGluGlyTyrSerTyrLeuValLysGluThrAspSerGluGlyTyrLysValLysVal 690

Db       1390 AGGAAAGATATAGAAGTATTATCCGAAGATACTGATTATGAAGAAGATGAAGTCACAAAA 1449

Qy        691 AsnSerGlnGluValAlaAsnAlaThrValSer--------------------------- 701

Db       1450 AAGAGAAAGGATGTCAAGAAGGACACAACAGATAAATCTTCAAAACCACAAATAAAACGT 1509

Qy        702 ----------------------------------LysThrGly--------------- 704

Db       1510 GGTAAAAGAAGGTATTGCAATACAGAAGAGTGTCTAAAAACTGGATCACCTGGCAAAAAG 1569

Qy        705 ---------IleThrSerAspGluThrLeuAlaPheGluAsnAsn--------------- 716

Db       1570 GAAGAGAAGGCCAAGAACAAAGAATCACTTTGCATGGAAAACAGTAGCAACAGCTCTTCA 1629

Qy        717 ---------------------LysGluProValValProThrGlyValAspGlnLysIle 729

Db       1630 GATGAAGATGAAGAAGAAACAAAAGCAAAGATGACACCAACT---------AAGAAATAC 1680

Qy        730 AsnGly 731

Db       1681 AATGGT 1686


Search completed: August 19, 2003, 19:47:04
Job time : 347 secs
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